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- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

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Search completed: February
Job time: 29.8333 secs
                   Hanzel DK,
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                       measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein #2449 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 28569; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21; DB 22; Length 74;
Pred. No. 4.2e+02;
0; Mismatches 0; Indels
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cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                        Penn SG, Hanzel DK, Chen W, Rank DR;
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                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                2000US-0180312.
2000US-0207456.
2000US-0608408.
                                                                                      03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234587.
04-OCT-2000; 2000GB-0024263.
30-JAN-2001; 2001WO-US00669
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Query Match
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Best Local 4; Conservative
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19 SYDA 22
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ò a (MOLE-) MOLECULAR DYNAMICS INC.

2000US-0632366. 2000US-0234687. 2000US-0236359.

21-SEP-2000; 27-SEP-2000;

2000GB-0024263

04-OCT-2000;

2000US-0207456 2000US-0608408

30-JUN-2000;

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6, 2003, 11:19:38

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed at fit, wipo.int/pub/published_pct_sequences.
                                                                                                                                                    Single exon nucleic acid probes for analyzing gene expression in human
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Rank DR
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   Chen W,
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Perfect score:
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1: /cgn2_6/ptodata/1,
2: //gn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: //gn2_6/ptodata/1,
5: //gn2_6/ptodata/1,
6: //gn2_6/ptodata/1,
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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    BB
                             US-08-310-912A-126

US-09-301-085-126

US-09-301-085-126

US-08-557-006C-19

US-08-630-915A-184

US-08-475-989-3

US-08-475-989-3

US-08-475-172-15

US-09-149-476-441

US-09-034-916-11

US-09-325-932A-181

US-09-325-932A-181

US-09-325-932A-181

US-09-325-932A-181

US-09-325-932A-111

US-09-325-932A-145

US-09-318-94A-2

US-09-318-793A-4

US-09-318-793A-4

US-09-318-793A-4

US-08-936-165A-462

US-08-936-165A-462

US-08-038-932B-1

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US-08-682-643-4
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Sequence 126, App
Sequence 126, App
Sequence 126, App
Sequence 19, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 117, App
Sequence 117, App
Sequence 117, Appl
Sequence 2, Appli
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Sequence 4, Appli
Sequence 46, Appli
Sequence 46, Appli
Sequence 46, Appli
Sequence 1, Appli
Sequence 5, Appli
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RESULT 1 US-08-310-912A-126 Sequence 126, Applica patent No. 5981730 GENERAL INFORMATION: Ausube APPLICANT: Ausube APPLICANT: Staska APPLICANT: Cantal Staska APPLICANT: MINDER OF SEQUENCE OF INVENTION NUMBER OF SEQUENCE APPLICANT: Windri APPLICANT: WINDER OF SEQUENCE OCORRESPONDENCE ADDRESSEE: FISH STATE: MA COUNTRY: USA ZIP: 02110-2904 COMPUTER READABLE MADDRESSEE: FISH STATE: MA COUNTRY: USA ZIP: 02110-2904 COMPUTER READABLE MADIUS SOFTWARE: Paten CURRENT APPLICATION NUMBER OF SEQUENCE APPLICATION NUMBER OF SEQUENCE CURRENT APPLICATION NUMBER OF SECUENCE SECUENCE OF SECUENCE SECUENCE CURRENT APPLICATION NUMBER FILING DATE: SECUENCE CAPPLICATION NUMBER SECUENCE CAPPLICATION NUMBER SECUENCE COUNTRY NEGRETIAND SOFTWART SECUENCE COUNTRY NEGRET APPLICATION NUMBER SECUENCE CHARACTER REGISTRATION NUMBER SECUENCE CHARACTER SECUENCE CHARACTER SECUENCE CHARACTER SECUENCE CHARACTER TOPOLOGY: linea signal substantion acidentic control of the secuence character processes of the secuence charac		200 200 200 200 200 200 200 200 200 200
912A-126 2 126 2 126		
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Leation US/083 N: Del, Frederic Kawicz, Brian Leation US/083 Deck, Douglas Girinos, Michae Guo-Ling CON: RPS2 GEN CON: RPS2 GEN CON: METHODS CES: 208 LDDRESS: Sh & Richards Tranklin Stree 104 LE FORM: Floppy disk Floppy disk Floppy disk Floppy disk Floppy disk Flopsy d		319 3419 3441 3441 3441 3748 4410 4410 4410 4410 4410 4410 4410 44
on US/0831 Frederick Cz, Brian Indrew F. Douglas Fundrew F. Douglas File Sene METHODS SS: Richardso lin Street US/08/3 Fundrew F. DATA: Sember 22, 36 Ember		34444222224215344
ion US/08310912A , Frederick M. ioz, Brian J. Andrew F. k, Douglas i, Funiaki Barbara N. os, Michael NLiang RPS2 GENE FAMILY, PRIMERS, PROBES METHODS SESS: 6 Richardson P.C. klin Street RICHARDS PROBES METHODS IN Release #1.0, Version #1.30B DATA: RR US/08/310,912A tember 22, 1994 536 DATA: RR 108/227,360 il 13, 1994 STATION: RF: 35,238 NUMBER: 00786/254001 NFORMATION: 1542-5070 42-8906 D NO: 126: STICS: acids	ALIGNMENTS	US-08-682-643-3 US-09-134-001C-5254 US-09-147-236-2 US-09-144-001C-4742 US-09-134-001C-4259 US-09-465-58-70 US-08-414-938A-4 US-08-472-172-6 US-08-472-172-6 US-08-472-172-2 US-09-004-838-127 US-08-578-709-15 US-08-457-274A-22 PCT-US95-05758-22 US-08-622-324-8 US-08-622-324-8 US-08-657-006C-40
S, AND DETECTION		Sequence 3, Appli Sequence 2, Appli Sequence 4742, Ap Sequence 4759, Ap Sequence 4259, Ap Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli Sequence 127, Appli Sequence 127, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 23, Appli Sequence 39, Appli Sequence 39, Appli Sequence 39, Appli Sequence 39, Appli

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CURRENT FILING DATE: 1999-04-28
EARLIER APPLICATION NUMBER: 08/310,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES,
TITLE OF INVENTION: DETECTION METHODS
FILE REFERENCE: 00786/254002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Brent, Andrew F. APPLICANT: Dahlbeck, Douglas APPLICANT: Katagiri, Fumiaki
                                                                                                                                                                                                                                                                                                                                                                       -US95-04589-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER FILING DATE: 1994-09-22
EARLIER APPLICATION NUMBER: 08/227,360
EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 208
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                                                                                        TITLE OF INVENTION.
NUMBER OF SEQUENCES: 201
CORRESPONDENCE ADDRESS:
CORRESPONDENCE Fish & Richardson
TORRESSEE: Fish & Richardson
TORRESSEE: TORRESSEE SUITE 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                     APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
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STATE:
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                                                    COUNTRY: USA
ZIP: 02110-2904
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Katagiri, Fumiaki
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Pred. No. 1.9e+05;
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Pred. No. 1.9e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein PCT-US95-04589-126
                                                                                                                                                                                                                                                   SOFTWARE: |
SEQ ID NO 19
                                                                Matches
                                                                                 Best
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Patent No. 6258547
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                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                            APPLICANT: Beri, Rajindar K.
APPLICANT: Carling, David
APPLICANT: Forder, Robert A.
TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
FILE REFERENCE: NAP/PH37588/UST
CURRENT APPLICATION NUMBER: US/08/557,006C
CURRENT FILING DATE: 1996-03-06
PRIOR APPLICATION NUMBER: PCT/GB94/01093
PRIOR APPLICATION NUMBER: PCT/GB94/01093
PRIOR FILING DATE: 1994-05-20
PRIOR FILING DATE: 1993-05-21
PRIOR FILING DATE: 1993-05-21
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: GB PRIOR FILING DATE: 1993-08-31
                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                  ORGANISM: Rat
                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: PCT/US95/04589
                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SYDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity les 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                               1 SYDA 4
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SYDA
                                                              4;
                                                                              Similarity
                                                                                                                                                                                                                                                                   PatentIn Ver. 2.1
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                                                                Conservative
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                                                         100.0%; Score 21; DI 100.0%; Pred. No. 30 tive 0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                            DB 4; Length 14; 30;
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RESULT 5

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US-08-930-605-15

: Sequence 15, Application US/08930605

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Best Local Similarity
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                                                                                                                                                                                                       GENERAL INFORMATION:
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TOPOLOGY: unl
MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: MCCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING
                                                                                                                                                     APPLICANT: ISHIKAWA, Y
APPLICANT: KUNO, Kouji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                          STREET: 3000
                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                          FITLE OF INVENTION:
                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 03-APR-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                             COUNTRY: U.S.A.
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                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                    1 SYDA 4
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                                                                            3000 K Street, N.W
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ISHIKAWA, Yuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAY, Brian K.
FOWLKES, Dana M.
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                                                                                          FOLEY & LARDNER
                                                                                                       ADDRESS:
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당 δÃ RESULT 7 US-08-475-989-3 US-08-930-605-15 Sequence 3, Patent No. Matches Best Query Match GENERAL INFORMATION: APPLICANT: CHONG, TELEFAX: (202) 672-539
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: COUNTRY: Canada
ZIP: M5G 1R7
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,989
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,839
FILING DATE: 03-FEB-1993 APPLICANT:
APPLICANT: REGIDITATION: 05: REFERENCE/DOCKET NUMBER: 05: TELECOMMUNICATION INFORMATION: (202) 672-5300 SOFTWARE: Patentin Rel CURRENT APPLICATION DATA: TITLE OF INVENTION: Synthetic Haemophilus Influenzae TITLE OF INVENTION: Conjugate Vaccine NUMBER OF SEQUENCES: 56 FILING DATE: 12-APR-1996 ATTORNEY/AGENT INFORMATION: FILING DATE: 13-APR-PRIOR APPLICATION DATA: CORRESPONDENCE ADDRESS: PRIOR APPLICATION DATA: MOLECULE TYPE: NUMBER OF SEQUENCES: APPLICANT: STREET: Suite 70 CITY: Toronto STATE: Ontario 10 SYDA 13 Local Similarity NAME: Wegner, Harold C. REGISTRATION NUMBER: 25 APPLICATION NUMBER: PCT/ FILING DATE: 12-APR-1996 APPLICATION NUMBER: JP 7-FILING DATE: 13-APR-1995 CLASSIFICATION: OPERATING SYSTEM: PC-DOS/MS-DOS TOPOLOGY: STRANDEDNESS FILING DATE: CLASSIFICATION: 1 SYDA 4 APPLICATION NUMBER: MEDIUM TYPE: ADDRESSEE: LENGTH: 25 amino acids 4; , Application US/08475989 5679352 amino acid Suite 701, KANDIL, Ali SIA, Charles 100.0%; Score 21; DB ilarity 100.0%; Pred. No. 55; Conservative 0; Mismatches KLEIN, Michel PatentIn Release #1.0, Version #1.30 linear IBM PC compatible Sim & McBurney peptide 14-OCT-1997 , Pele 672-5399 330 University Avenue JP 7-111033 PCT/JP96/01028 US/08/930,605 25,258 053466/0215 DB 2; Length 25; 0; Indels 0 Gaps

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APPLICATION NUMBER:

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US-08-475-985-3
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                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA93/00041
FILING DATE: 03-FEB-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9202219.3
FILING DATE: 03-FEB-1992
CLASSIFICATION: 424
APPLICATION: 424
APPLICATION: 424
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APPLICANT: CHONG, Pele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
CLASSIFICATION. ... ATTORNEY/AGENT INFORMATION: NAME: STEWART, MICHAEL I.
                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,985
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,839
FILING DATE: 03-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Synthetic TITLE OF INVENTION: Conjugate NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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APPLICATION NUMBER:
FILING DATE: 03-FEB-
                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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TYPE: amino acid
STRANDEDNESS: single
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Suite 701, 330 University Avenue
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SIA, Charles
KLEIN, Michel
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linear
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                                                                                                                                                                        PCT/CA93/00041
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Vaccine
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RESULT 9
US-08-472-172-15
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                                                                                                                                                                                                SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,172
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/849,411
FILING DATE: 07-UL-1992
CLASSIFICATION: 435
APTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
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Matches 4; Conserv
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                                                                             TELEFAX: (416) 595-11
TELEX: 063-24567 SIMB
INFORMATION FOR SEQ ID NO:
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                           SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
                                                                                                                      NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
APPLICANT:
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LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Suite
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: Canada
ZIP: M5G 1R6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Sim & McBurney | Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08472172
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(416) 59
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Klein, Michel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grass,
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linear
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              single
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                                                                                            SIMBAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outer Membrane Protein P1 and Peptides of Haemophilus Influenzae Type B
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Pred. No.
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US-09-149-476-441

Sequence 441 Application US/09149476

Patent No. 6420526

GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0%; Pred. No. 79; Matches 4; Conservative 0; Mismatches
   APPLICATE ROSEN et al.
APPLICATE ROSEN et al.
TITLE OF INVENTION 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1998-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: 3:
 EARLIER APPLICATION NUMBER: 60/040,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUTICATION INFORMATION:
TELEPHONE: (416) 595-1155
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LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
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ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,839
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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STATE: Ontario
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SIA, Charles
KLEIN, Michel
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Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                           100.0%; Score 21; DB 3;
100.0%; Pred. No. 79;
tive 0; Mismatches 0
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ER FILING DATE: 1997-05-23
ER FILING DATE: 1997-05-3
ER FILING DATE: 1997-05-3
ER APPLICATION NUMBER: 60/047,633
ER FILING DATE: 1997-05-23
ER FILING DATE: 1997-05-23
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,617
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,618
ER APPLICATION NUMBER: 60/047,618
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,618
ER FILING DATE: 1997-05-23
                                                                                                     R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,314
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,569
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,311
R FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R APPLICATION NUMBER: 60/047,581
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,584
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,500
R FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R APPLICATION NUMBER: 60/04
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/04
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/04
R FILING DATE: 1997-05-23
                                APPLINGATION NUMBER: 60/043,671
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,674
FILING DATE: 1997-04-11
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/047,600
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APPLICATION NUMBER: 60/
FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/040,334 FILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-04-11
                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/043,568
                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/043,580 FILING DATE: 1997-04-11
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                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/047,632 FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,612
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,582
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,596
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FILING DATE: 1997-03-07
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R APPLICATION NUMBER: 60/04
R FILING DATE: 1997-05-23
RR APPLICATION NUMBER: 60/04
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/04
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IR APPLICATION NUMBER: 60/056,882
IR FILING DATE: 1997-08-22
IR APPLICATION NUMBER: 60/056,637
IR FILING DATE: 1997-08-22
IR APPLICATION NUMBER: 60/056,903
IR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR APPLICATION NUMBER: 60,056,893
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60,056,630
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60,056,878
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60,056,662
ER FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,910
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,864
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APPLICATION NUMBER: 60/056,894
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,879
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,877
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/
FILING DATE: 1997-04-11
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FILING DATE: 1997-08-22
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/
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                                    60/047,594
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RESULT 12
US-09-034-916-11
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Best Local S
Matches 4
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                                                                                                                                             GENERAL INFORMATION:

APPLICANT: GEBE, JOHN A.

APPLICANT: SIDAK, ANTHONY W.

APPLICANT: ARUFFO, ALEJANDRO A.

TITLE OF INVENTION: SPALPHA: A NOVEL SCAVENGER RECEPTOR

TITLE OF INVENTION: CYSTEINE-RICH DOMAIN-CONTAINING POLY

TITLE OF INVENTION: ANTHODIES THERETO

NUMBER OF SEQUENCES: 17
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COMPUTER READABLE FORM:
                                                                                                                           CORRESPONDENCE ADDRESS:
                                                     CITY: MENLO PARK
STATE: CALIFORNIA
                                                                        ADDRESSEE: RUBLING - STREET: 90 MIDDLEFTELD
                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                     35 SYDA
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FR APPLICATION NUMBER: 60/056,908

FR FILING DATE: 1997-08-22

FR APPLICATION NUMBER: 60/048,964

FR FILING DATE: 1997-06-06

FR APPLICATION NUMBER: 60/057,650
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ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,881
ER APPLICATION NUMBER: 60/056,909
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,875
ER APPLICATION NUMBER: 60/056,875
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,862
ER FILING DATE: 1997-08-25
ER FILING DATE: 1997-08-25
ER APPLICATION NUMBER: 60/056,862
ER APPLICATION NUMBER: 60/056,862
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ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/043,670
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/056,632
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-28
ER FILING DATE: 1997-08-28
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PR FILING DATE: 1997-05-23
PR APPLICATION NUMBER: 60/047,614
PR FILING DATE: 1997-05-23
PR APPLICATION NUMBER: 60/043,576
PR APPLICATION NUMBER: 60/043,576
PR APPLICATION NUMBER: 60/043,576
PR FILING DATE: 1997-04-11
PR FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/056,884
APPLICATION NUMBER: 70/056,884
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FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/
FILING DATE: 1997-10-02
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APPLICATION NUMBER: 60/057,669
FILING DATE: 1997-09-05
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: 1997-10-02
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NUMBER: 60/047,593
                                                                                  & ASSOCIATES |
FIELD ROAD, SUITE
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Gaps

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; TYPE: PRT ; ORGANISM: Pinus radiata US-09-325-932A-181
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                                                                                                      US-09-325-932A-177
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LENGTH: 132
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APPLICANT: Filnn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant devel
FILE REFERENCE: 1022
                                                    Sequence 177, Application US/09325932A Patent No. 6451604 GENERAL INFORMATION:
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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 APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compos
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60
FILING DATE: 06-MAR-1997
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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SOFTWARE: PatentIn Release #1.0
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COMPUTER: IF
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Compositions affecting programmed cell
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RESULT 16
US-09-325-932A-145
; Sequence 145, Application US/09325932A
; Patent No. 6451604
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US-09-615-192A-275
: Sequence 275, Application US/09615192A
; Patent No. 6410718
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SEQ ID NO 177
LENGTH: 133
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 145
LENGTH: 204
TYPE: PRT
                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lesham, Annette
APPLICANT: Lesham, Composi
TITLE OF INVENTION: Composi
TITLE OF INVENTION: death a
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PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin (
FILE REFERENCE: 11000.1003c4U
CURRENT FILING DATE: 2000-07-12
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                          78 SYDA
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                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for Windows Version 3.0
                                                                                                                                           Compositions affecting programmed cell death and their use in the modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     death and their use in the modification of forestry plant dev
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 160;
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                                                                                                                                           of forestry plant
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US-09-286-690-2

; Sequence 2, Application US/09286690

; Patent No. 6103511
                                                                                                        RESULT 18
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US-08-578-709-11
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GENERAL INFORMATION:
APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars
                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/578,709
FILING DATE: 28-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/JP95/00838
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: JP 114316/1994
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gubinsky Ionis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Applicat Patent No. 5814509
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202)293-7860 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Gubinsky, Louis
REGISTRATION NUMBER: 24,835
REFERENCE/DOCKET NUMBER: Q4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TANABE, Tadashi
TITLE OF INVENTION: PROSTACYCLIN SYNTHASI
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEA
STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                         82 SYDA 85
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Washington
STATE: D.C.
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100.0%; F
tive 0;
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                                                                                                                                                                                                                                  Score 21; DB 2;
Pred. No. 5.9e+02;
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Pred. No.
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RESULT 20
US-09-318-793A-4
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; TYPE: PRT
; ORGANISM: Orpinomyces sp. PC-2
US-09-286-690-2
CURRENT APPLICATION NUMBER: US/09/318,793A
CURRENT FILING DATE: 1999-05-26
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
LENGTH: 271
TYPE: PRT
                                                                                                                                                                                                                                     Sequence 4, Application US/09318793A Patent No. 6184007 GENERAL INFORMATION:
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GENERAL INFORMATION:
                                                                                                    APPLICANT: Dusch, Nicole
APPLICANT: Kalinowski, Jorn
APPLICANT: Kalinowski, Jorn
APPLICANT: Puhler, Alfred
TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC
TITLE OF INVENTION: ACID BY ENHANCEMENT OF THE pand GENE IN MICROORGANISMS
FILE REFERENCE: 21123/260204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local :
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Matches
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SEQ ID NO 2
LENGTH: 245
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CURRENT APPLICATION NUMBER: US/09/318,794A
CURRENT FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: DE 198 55 312.9
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DEGUSSA AKTIENGESELLSCHAFT
TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC
TITLE OF INVENTION: ACID USING CORVNEFORM BACTERIA
FILE REFERENCE: eggeling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/286,690
CURRENT FILING DATE: 1999-04 05
EARLIER APPLICATION NUMBER: US 60/027,882
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: PCT/US97/17811
EARLIER APPLICATION NUMBER: PCT/US97/17811
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Lichenase and Coding Sequences
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Pred., No. 6.8e+02;
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Pred: No. 6.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 271;
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; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5603
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US-09-134-001C-5603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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SEQ ID NO 5603
LENGTH: 287
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                             tent No. 634858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Corynebacterium glutamicum
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                             TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides TITLE OF INVENTION: Polypeptides and Their Uses
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                                                                                                           STREET:
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                                                                        COUNTRY:
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                                                                                                       King of Prussia
                                                                                            PA
                                                                                                                                                                                                                                Reichard, Richard
Rosenberg, Martin
Ward, Judith
                                                                        USA
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                                                                                                                                                                                                                                                                                                                     Knowles, David
Lonetto, Michael
                                                                                                                                                                                                                                                                                    Pratt, Julie
                                                                                                                                                                                                                                                                                                   Nicholas, Richard
                                                                                                                                                                                                                                                                                                                                                      Burnham, Martin
Hodgson, John
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IBM Compatible
                     Diskette
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pred. No. 7.2e+02;
pred. No. 7.2e+02;
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RESULT 23
US-08-038-932B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPGTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-
FILING DATE: 08-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                             ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 SYDA 189
                                                                                                                                                                                                                                                                                     STREET: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                        STATE: Washington, D.C. COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 100.0%; Score 21; I Local Similarity 100.0%; Pred. No. 7 Local Similarity 00, Mismatches 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1,
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APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                        INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08038932B
                                                                                                                                                                                                                                                                                                          1100 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 amino acids
                                                                                                                                                                                                                                                                                                                                                                                    Wada, Akiyoshi
                                                                                                                                                                                                                                                                                                                                                                                               Endo, Kimiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yoneya, Takashi
Miyake, Toshio
Aoyama, Atsuo
                                                                                                                                                                                                                                                                                                                                                                                                                  Kidokoro, Shun-ichi
Miki, Yoichiro
                                                                                                                                                                                                                                                                                                                                                                                                                                               Kai, Ken-ichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagao, Hiromasa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bs: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                          Cushman, Darby & Cushman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
        UMBER: JP 4-237606
14-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                       NOVEL PROTEASE
                                                                                                                                     US/08/038,932B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/936,165A
                                                                         JP 4-171479
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RESULT 25
US-08-682-643-4
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                                                                                                                                                                       Sequence 4, Application US/08682643 Patent No. 6103512 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                          Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-638-4203
TELEX: 248453
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2" 1.44 Mb Floppy diskette
COMPUTER: IBM 486/DX100 ValuePoint PC
                                                                                                              TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 202-861-3000
                   OPERATING SYSTEM: Microsoft OPERATING SYSTEM: Version 4
                                                                                                                                                                                                                                                                                   65 SYDA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 amino acids
                                                                                                                    Venema, Gerhardus; Eijsink, Vincentius
VENTION: Thermostable Variants of Neutral
VENTION: Proteases of Bacillus Stearothermophilus and
                                                                                                                                                                                                                                                                                                                                           Conservative
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       PatentIn
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100.0%; P
ative 0;
                                                                                                         Bacillus Thermoproteolyticus
                                 Microsoft Windows
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100.0%; Pred. No. 8e+02;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      Score 21;
Pred. No.
#1.0 Version #1.30 (EPO),
                                                                                                                                                                                                                                                                                                                                          Mismatches
                                 NT Workstation
                                                                                                                                                                                                                                                                                                                                                     8e+02;
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RESULT 26
US-09-104-623A-5
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TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (908)530-6584
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROZEC, CATOL
REGISTRATION NUMBER: 36,993
                               TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 63037
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Olsen, Arne Agerlin
APPLICANT: Fatum, Tine Muxoll
APPLICANT: Deussen, Heinz-Josei
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Roggen, Erwin Ludo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFFIANCE
FILING DATE: 27-JAN-ya
ATTORNEY/AGENT INFORMATION:
NAME: Michaelson, Peter L.
NAME: Michaelson, Peter L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30090
REFERENCE/DOCKET NUMBER: RI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)530-6671
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                      CITY:
STATE:
                            TELEPHONE:
                                                                                                                                             APPLICATION NUMBER: FILING DATE: 25-JUN
                                                                                                                                                                                                                                                                        ZIP:
                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                     COUNTRY:
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STRANDEDNESS: unl
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                                                                                                                                                                                                                                                                        10174
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                                                                                                                                                                                                                                                                                                                                 405 Lexington
                   212-878-9655
                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                   No. 63037520 No.
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4: 435
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                                                                                                                                                         us/09/104,623A
                                                                                                                                                                                                                                                                                                                                                                                            Modified Polypeptide
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                                                             5256.200<sub>1</sub>-us
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GENERAL INFORMATION:

APPLICANT: Olsen, Arne Agerlin

APPLICANT: Olsen, Annette

TITLE OF INVENTION: A Modified Enzyme for Skin Care

FILE REFERENCE: 4922.204-US

CURRENT APPLICATION NUMBER: US/09/019,532B

CURRENT FILING DATE: 1998-02-05

EARLIER APPLICATION NUMBER: 0038/97

EARLIER FILING DATE: 1997-01-10

EARLIER FILING DATE: 1997-01-07

EARLIER FILING DATE: 1997-06-25

EARLIER APPLICATION NUMBER: 60/051,381

EARLIER APPLICATION NUMBER: 60/051,381
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SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 316
TYPE: PRT
ORGANISM: Bacillus thermoproteolyticus
US-09-019-532-5
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; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; STRAIN: Bacillus Thermoproteolyticus
US-09-104-623A-5
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US-08-682-643-3
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Matches
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SOFTWARE: PatentIn Release #1.0 version SOFTWARE: and Windows No. 6103512epad CURRENT APPLICATION DATA:
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2° 1.44 Mb Floppy diskette
COMPUTER: IBM 486/DX100 ValuePoint PC
OPERATING SYSTEM: Microsoft Windows NT Workstation
OPERATING SYSTEM: Version 4
                                                                                                                                                                                APPLICANT: Venema, Gerhardus; Eijsink, Vincentius
TITLE OF INVENTION: Thermostable Variants of Neutral
TITLE OF INVENTION: Proteases of Bacillus Stearothermophilus and
TITLE OF INVENTION: Bacillus Thermoproteolyticus
                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                          65 SYDA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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Local Similarity 100.
Local Similarity 100.
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SYDA 4
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                                               PatentIn Release #1.0 Version #1.30 (EPO),
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1997-07-07
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100.0%; P
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Pred. No. 8e+02;
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Pred. No.
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8e+02;
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RESULT 30
US-09-147-236-2
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5254
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US-09-134-001C-5254
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APPLICANT: LYIN DOUCETTE-Stamm et al
APPLICANT: LYIN DOUCETTE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5254
Sequence 2, Application US/09147236A Patent No. 6316251
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                                                                                                                                                  Matches
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (908)530-6584 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 27-JAN-94
ATTORNEY/AGENT INFORMATION:
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
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                                                                                        265 SYDA 268
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STRANDEDNESS: unl
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REGISTRATION NUMBER: 30090
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                                                                                                                   1 SYDA 4
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NO
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Pred. No.
                                                                                                                                                             Score 21; DB 4;
Pred. No. 8.4e+02;
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GENERAL INFORMATION:

APPLICANT: TONOUCHI, Naoto APPLICANT: TSUCHIDA, Takayasu APPLICANT: YOSHINAGA, Fumihir

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RESULT 32
US-09-134-001C-4259
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           GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
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APPLICANT: LYND DOUCETTE-Stamm et al
APPLICANT: LYND DOUCETTE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PELING DATE: 1997-10-05
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER DE GEO TO NOCE FEEL 1997-08-14
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LENGTH: 348
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Best Local
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LENGTH: 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Acetobacter xylinum
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ID NOS: 5674
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Pred. No.
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Pred. No.
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RESULT 34
US-08-414-938A-4
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US-09-465-558-70
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Best Local S
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LENGTH: 376
SOFTWARE: Patentin Release #1.0, vecurrent application Data:
APPLICATION UMBER: US/08/414,938A
FILING DATE: March 31, 1995
CLASSIFICATION: 800
ATTORNEY/ACENT INFORMATION:
NAME: JOHN P. WHITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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APPLICANT: LAGUDAH,
TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MOTAKINYO, LAYO O.
APPLICANT: OTOZGO JI, EMIL M.
TITLE OF INVENTION: TETRAHYDROFOLATE METABOLIC ENZYMES
FILE REFERENCE: BB1322 US NA
CURRENT APPLICATION NUMBER: US/09/465,558
CURRENT FILING DATE: 1999-12-17
EARLIER APPLICATION NUMBER: 60/112,734
EARLIER FILING DATE: 1998-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 SYDA 385
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                                                                                                                                                                                                        CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                            ZIP: 10036
                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                       UNITED STATES OF AMERICA
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                                                                                                                                                                                                                                                                                            EVANS SYLVANUS |
GENETIC SEQUENCES CONFERRING
NEMATODE RESISTANCE IN PLANTS
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                                                             US/08/414,938A
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Pred. No. 1e+03;
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                                                                                            Version #1.25
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; STRANDEDNESS: not rel; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-945-848-8
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US-08-945-848-8
RESULT 36
US-08-472-172-6
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                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAWLey, Jr, Thomas A.
REGISTRATION NUMBER: 40,944
REFERENCE/DOCKET NUMBER: 1903
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPEAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08945848 Patent No. 5968772 GENERAL INFORMATION:
                                                                                                                                      Matches
                                                                                                                                                    Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 0687/47527/JPW/GJG TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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293 SYDA 296
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                   71 SYDA 74
                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                                                                                                       430 amino acids
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VENTION: PEARL PROTEIN(NACREIN) AND PROCESS FOR
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100.0%; Pred. No. 1.1e+03;
htive 0; Mismatches 0;
                                                                                                                                                  100.0%; Score 21; DB 2; 100.0%; Pred. No. 1.1e+03;
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Best Local Similarity
Thehes 4; Conserv
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                                                                                                                                                           Sequence 4, Application US/08472172 Patent No. 5985288 GENERAL INFORMATION:
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                                                                              APPLICANT:
APPLICANT:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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PRIOR APPLICATION DATA:
07/849,411
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SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,172
FILING DATE: 07-JUN-1995
TITLE OF INVENTION: Outer Membrane Protein P1 and Peptides TITLE OF INVENTION: of Haemophilus Influenzae Type B NUMBER OF SEQUENCES: 26
                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
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TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 249
REFERENCE/DOCKET NUMBER:
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                                               APPLICANT:
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                                                                                                                                                                                                                                                                              144 SYDA 147
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                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
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                                            Chong, Pele Y Y
Fahim, Raafat
Sia, Charles D Y
McVerry, Patrick
Klein, Michel
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                                                                                                                            Munson, Jr.,
Grass, Susan
                                                                                                                                                                                                                                                                                                                                        100.0%; Score 21; DB 2; ilarity 100.0%; Pred. No. 1.1e+03; Conservative 0; Mismatches 0;
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Chong, Pele Y Y
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Klein, Michel
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ite 701, 330 University Avenue
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Type B
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/849
FILING DATE: 07-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REGISTRATION NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1055-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (416) 595-1163
TELEX: 063-24567 SIMBAS
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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LENGTH: 455 amino acids
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PRIOR APPLICATION DATA:
07/849,411
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,172
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                     TITLE OF INVENTION: Outer Membrane Protein P1 and Peptides TITLE OF INVENTION: of Haemophilus Influenzae Type B NUMBER OF SEQUENCES: 26
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CITY: Toronto
STATE: Ontario
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                                                                                          COUNTRY: Canada
ZIP: M5G 1R6
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STRANDEDNESS: sir
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ZIP: M5G 1R6
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Suite 701, 330 University Avenue
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Suite 701, 330 University Avenue
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McVerry, Patrick
Klein, Michel
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Fahim, Raafat
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Patent No.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                         NAME: Einhorn, Gregory P. 40
REGISTON NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                   FILING DATE: 09-JAN-1
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/849,411
                                                                                                                                                        APPLICATION NUMBER: US 0
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Michelmore, Richard W. |
APPLICANT: Shen, Kathy
APPLICANT: Weyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 459 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELECHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 SYDA 151
                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Two warmer CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (416) 595-1163
TELEFAX: (416) 595-1163
TELEX: 063-24567 SIMBAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0: FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Stewart, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 07-JUL-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127, Application US/09004838 |
5. 6350933 |
                                                                                                                                                                                                                                                                                                                                                                                                                         94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 21; DB 2; illarity 100.0%; Pred: No. 1.2e+03; Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                              09-JAN-1998
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-578-709-15
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Matches
                                                                                         Query Match
                                                              Matches
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                                                                                                                                                                                           TELEFAX: (202)293-7850
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: Q4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
US/08/578,709
APPLICATION NUMBER: US/08/578,709
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/JP95/00838
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 114316/1994
FILING DATE: 28-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/JP95/00838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Gubinsky, Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                         Local Similarity
 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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                                                                                                                                                                                   LENGTH:
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                              1 SYDA 4
SYDA 85
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                                                                                                                                                                   amino acid
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                                                                                                                                                                                   500 amino acids
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                                                            Conservative
                                                                                                                                                                                                                                (202)293-7860
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100.0%; P
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100.0%; F
tive 0;
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                                                                                                                                                                                                                                                                                          24,835
                                                                                                                                                                                                                                                                              Q40439
                                                                         Score 21; DB 2;
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 4;
Pred. No. 1.3e+03;
                                                            Mismatches
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                                                           0;
                                                                                        Length 500;
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RESULT 41

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; CHROMOSOME/SEGMENT: Chromosome 5
US-08-457-274A-22
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                                                                                                                                                                                           Sequence 22, Application PC/TUS9505758 GENERAL INFORMATION:
APPLICANT: Cornell Research Founda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application US/08457274A Patent No. 5734086
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
COMPUTER READABLE FORM:
                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 507 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Scott, Jeffrey G. APPLICANT: Tomita, Takashi TITLE OF INVENTION: Cytochro
                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 716-263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                 348 SYDA 351
                                             ADDRESSEE: Nixon, Hargrave, Devans & ESTREET: P.O. Box 1051, Clinton Square CITY: Rochester STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: /+ - TELEPHONE: /+ - TELEPHONE: /16-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN: Rutgers
DEVELOPMENTAL STAGE: Adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rochester
STATE: New York
                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity es 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                  1 SYDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Nixon, Hargrave, Devans & Doyle P.O. Box 1051, Clinton Square
                                                                                                                                                                         Cornell Research Foundation, Inc. VENTION: Cytochrome P4501pr Gene and
                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 21; DB 1; 100.0%; pred. No. 1.3e+03; Migmatches 0;
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                                                                                                     Devans & Doyle
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 507;
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MEDIUM TYPE: COMPUTER: II

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COUNTRY: US
CIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,324
FILING DATE: 21-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/013,945
PRIOR APPLICATION NUMBER: US 60/013,945

**TING DATE: 22-MAR-1996

**TING DATE: 22-MAR-1996
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US-08-822-324-8
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Best Local Similarity 100.
Thes 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08822324
Patent No. 6129917
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Travis, James
APPLICANT: Genco, Caroline A.
TITLE OF INVENTION: IMMUNOGENIO
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 507 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: pro
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: Adult POSITION IN GENOME: CHROMOSOME/SEGMENT: Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION: 716-263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: GOLdman, Michael L.
REGISTRATION NUMBER: 30,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 SYDA 351
                                                                                                                                                                                                                                                                                                                                                CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polon-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN: Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                              E: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potempa, Jan S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Musca domestica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMUNOGENIC COMPOSITIONS COMPRISING PEPTIDES AND PORPHYROMONAS GINGIVALIS PROTEINS AND/OR PEPTIDES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 21; DB 5; I 100.0%; Pred. No. 1.3e+03; tive 0; Mismatches 0;
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US-09-066-046-39; Sequence 39, Application in Patent No. 6204252; Patent No. 6204252; GENERAL INFORMATION:
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Query Match
Best Local Similarity 100.
Thes 4; Conservative
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                                                                                                                                                                REGISTRATION NUMBER: 39,850
REFERENCE/DOCKET NUMBER: 106.4
TELECOMMUNICATION INFORMATION: |
TELEPHONE: (617) 526-6000 |
TELEPHONE: (617) 526-5000
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 545 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 488-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: li
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                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/066,046A
FILING DATE: 24-Apr-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk |
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release | #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: CHARACTERIZATION OF GRANULOCYTIC EHRLICHIA AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MURPHY, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09066046A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 21; DB 3; 1 ilarity 100.0%; Pred. No. 1.3e+03; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BELTZ, Gerald A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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                                            100.0%;
                         100.0%; Score 21; DE 100.0%; Pred. No. 1.4 ive 0; Mismatches
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                                          1.4e+03;
                                                                DB 4;
                                                            Length 545;
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Sequence 40, Application US/OB557006C

Sequence 40, Application US/OB557006C

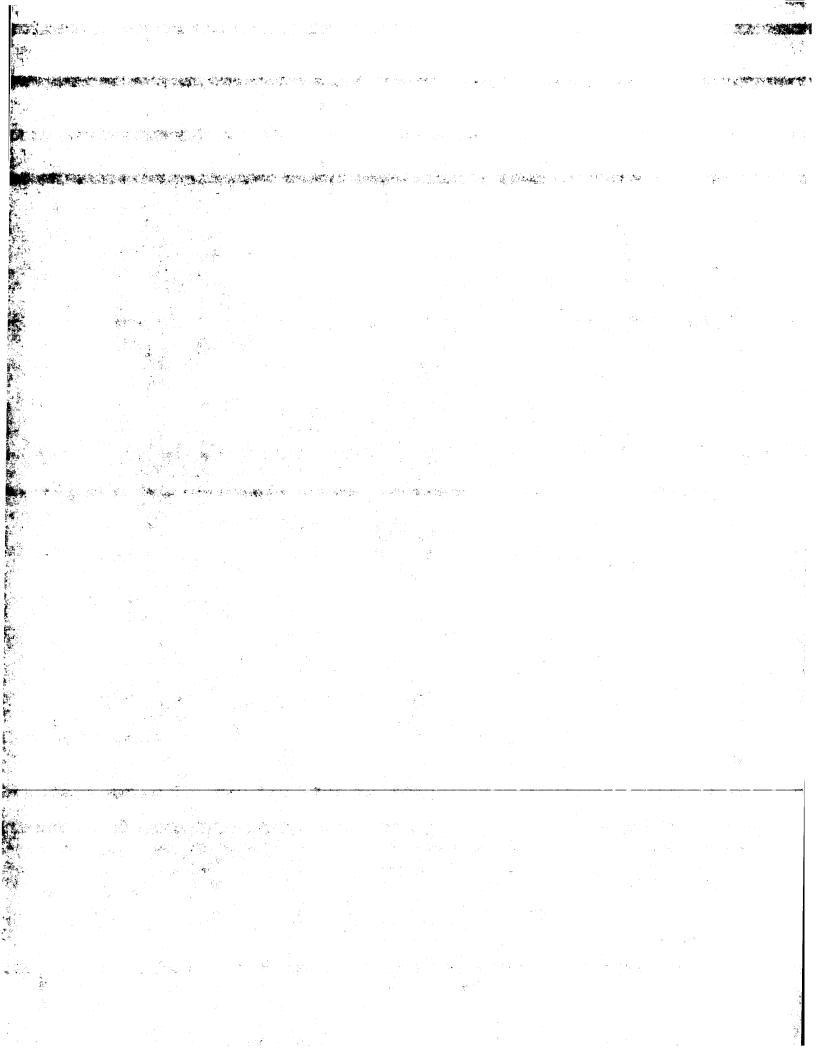
Patent No. 628547

GENERAL INCOMMITON:
APPLICANT: Beril Rajindar K.
APPLICANT: Carling David K.
APPLICANT: Porder Robert M.
APPLICANT: Porder Robert M.
APPLICANT: PROPERTION NUMBER: US/OB/S57,006C
CORRENT FILING DATE: 1956-03-06
PRIOR APPLICATION NUMBER: US/OB/S57,006C
CORRENT FILING DATE: 1936-03-05-21
PRIOR FILING DATE: 1936-05-21
PRIOR FILING DATE: 1936-06-31
NUMBER OF SEQ ID NOS: 44
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 40
LENGTH: 552
PRIOR FILING DATION: Fill length cDNA sequence fragment of Human AMPK - OTHER INFORMATION: Fill length CDNA sequence fragment of Human AMPK - OTHER INFORMATION: Incleotide 1765
US-OB-S57-006C-40

Query Match
Dougleted: February 6, 2003, 11:24:06

Search completed: February 6, 2003, 11:24:06

Search completed: February 6, 2003, 11:24:06
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Result
No.
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Maximum DB
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Perfect score:
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    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_AA: *
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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      6, 2003, 11:22:09; Search time 5.83333 Seconds
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   10 US-09-867-852-126

10 US-09-879-957-184

10 US-09-864-761-34093

11 US-09-864-761-35948

11 US-09-864-761-35948

12 US-09-864-761-42544

13 US-09-864-761-47595

14 US-09-864-761-47595

10 US-09-864-761-47709

20 US-09-796-692-1351

21 US-09-970-088-11

21 US-09-970-088-12

21 US-09-970-088-13

21 US-09-970-088-14

21 US-09-970-088-14

22 US-09-970-088-14

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24 US-09-970-088-14

25 US-09-970-088-14

26 US-09-970-088-14

27 US-09-970-088-14

28 US-09-970-088-14

29 US-09-3864-761-39939

27 US-09-3864-761-39939

27 US-09-38626-6309
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15.202 Million cell updates/sec
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   Sequence 4419,
Sequence 6309,
Sequence 5341,
Sequence 1351 Appl
Sequence 12 Appl
Sequence 13 Appl
Sequence 13 Appl
Sequence 306 Appl
Sequence 306 App
Sequence 3939, A
Sequence 4419, Ap
Sequence 4309 Ap
Sequence 5391 Ap
                                                                                                                                                                  Sequence 126, App
Sequence 184, App
Sequence 34093, A
Sequence 34172, A
Sequence 39908, A
Sequence 35748, A
Sequence 42544, A
Sequence 47595, A
Sequence 47595, A
                                                                                                                                                                                                                                                                                                                                          Description
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US-09-824-735-4	US-09-925-302-477	US-09-815-242-11757	US-09-815-242-5045	US-09-820-893-56	US-09-815-242-5696	US-09-971-536-60	US-09-738-626-5738	US-09-815-242-11378	US-09-738-626-5241	US-09-799-777-45	US-09-888-615-95	US-09-808-602-105	US-09-738-626-4252	US-09-815-242-10844	US-09-815-242-10953	US-09-962-618-2	US-09-738-626-4308	US-09-808-602-106	US-09-939-980-462	US-09-738-626-3633	US-09-808-602-101	US-09-808-602-25	US-09-808-602-23	US-09-993-308-2	US-09-925-299-958
Sequence 4, Appli	Sequence 477, App	Sequence 11757, A	5045	Sequence 56, Appl	Sequence 5696, Ap	Sequence 60, Appl	Sequence 5738, Ap	78	241,		Sequence 95, Appl	Sequence 105, App	-	Sequence 10844, A	Sequence 10953, A	(D	Sequence 4308, Ap	90,	Sequence 462, App	3633	ŗ	Sequence 25, Appl	Sequence 23, Appl	Sequence 2, Appli	Sequence 958, App

ALIGNMENTS

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PRIOR APPLICATION NUMBER: 2001-05-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085

PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-22

PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360

PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13

NUMBER OF SEQ ID NOS: 208

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 126

LENGTH: 7

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                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-867-852-126
В
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; Patent No. US20020147324A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
                                                                              Matches
                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS3 GENE FAMILY, PRIMERS, PROBES, AND
TITLE OF INVENTION: DETECTION METHODS
FILE REFERENCE: 00786/254002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: APPLICANT:
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SYDA
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Mindrinos, Michael N.
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Katagiri, Fumiaki
                                                                                Conservative
                                                                                                 100.0%;
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                                                                              Score 21; DB 10;
Pred. No. 1.1e+05;
; Mismatches 0;
                                                                                                                    Length 7;
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RESULT

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RESULT 3
US-09-864-761-34093
US-09-864-761-34093, Application US/09864761
Patent No. US20020048763A1
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                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 184: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                             1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 22 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/630,915 FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
ULE TYPE: peptide
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llarity 100.0%;
Conservative 0;
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INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
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US-09-864-761-34172
; Sequence 34172, Application US/09864761
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     GENERAL INFORMATION:
APPLICANT: Penn, Sh
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Best Local :
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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NUMBER OF SEQ ID NOS: 49117
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0663
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ORGANISM: Homo sapiens
FEATURE:
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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Penn, Sharron G.
Rank, David R.
                                                                                                                                                                                                                                                                                                                                          Conservative
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NN EXPRESSED IN HEART, SIGNAL = 0.86

NN EXPRESSED IN BT474, SIGNAL = 2.8

NN EXPRESSED IN BONE MARROW, SIGNAL = 2.8

NN EXPRESSED IN HELA, SIGNAL = 1.1

NN EXPRESSED IN HELA, SIGNAL = 1.9

NN EXPRESSED IN HELIOO, SIGNAL = 1.9

NN EXPRESSED IN HELIOO, SIGNAL = 1.4

NN EXPRESSED IN FETAL LIVER, SIGNAL = 1.4

NN EXPRESSED IN LUNG, SIGNAL = 1.4
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Pred. No. 78;
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 34172
LENCTH: 65
TYPE: PRT
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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ITTLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ITTLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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36
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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ED IN ADULT LIVER, SIGNAL = 1.4
ED IN PLACENTA, SIGNAL = 1.2
ED IN HEART, SIGNAL = 1.2
ED IN HEARI, SIGNAL = 1.5
ED IN HBL100, SIGNAL = 1.3
ED IN LUNG, SIGNAL = 1.3
ED IN BONE MARROW, SIGNAL = 2.7
AN HIT: AW937895.1, EVALUE 1.00e-16
OT HIT: P22415, EVALUE 3.00e-17
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US-09-864-761-39908
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US-09-864-761-39908
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LENGTH: 65
TYPE: PRT
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CURRENT FILING DATE: 2001-05-23
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NUMBER OF SEQ ID NOS: 49117
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APPLICATION NUMBER: US 60/236,359
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N: EXPRESSED IN LUNG, SIGNAL = 1.5

N: EXPRESSED IN PLACENTA, SIGNAL = 1.3

N: EXPRESSED IN HEARP, SIGNAL = 1.5

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4

N: EXPRESSED IN BRAIM, SIGNAL = 1.4

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

N: EXPRESSED IN HELA, SIGNAL = 1.8

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
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                                                                             H BONE MARROW, SIGNAL = 1.2

H HELA, SIGNAL = 1.8

I ADULT LIVER, SIGNAL = 1.5

T: AW503913.1, EVALUE 1.00e-29

T: P33892, EVALUE 4.00e-08
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                 Length 65;
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Query Match Best Local Similarity

Score Pred.

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NUMBER OF SEQ ID NOS: 49117
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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OR FILING DATE: 2000-10-04
OR APPLICATION NUMBER: US 60/236,359
OR FILING DATE: 2000-09-27
OR APPLICATION NUMBER: PCT/US01/00666
OR APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
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APPLICATION NUMBER: US 09/774,203
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APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: PCT/US01/00662
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                 TO AL035705.14
ESSED IN HEART, SIGNAL = 2.1
ESSED IN BRAIN, SIGNAL = 0.91
ESSED IN LUNG, SIGNAL = 8.7
ESSED IN FETAL LIVER, SIGNAL = 1.5
ESSED IN HELA, SIGNAL = 1.8
ESPROT HIT: Q09137, EVALUE 8.00e-40
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HIT: BE677760.1,
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Best Local :
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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OTHER INFORMATION: MAP TO AL035705.22'
OTHER INFORMATION: EXPRESSED IN ADULT! LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: SWISSPROT HIT: Q09137, EVALUE 8.00e-40
OTHER INFORMATION: EST_HUMAN HIT: BE677760.1, EVALUE 1.00e
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PRIOR FILING DATE: 2000-08-03
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2000-06-30
US 09/774,203
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     EVALUE 1.00e-29
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                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEO ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEO ID NO 47595
LENGTH: 74
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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PEATURE:
PEATURE:
OTHER INFORMATION: MAP TO AL035705.16
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.97
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                                                                                                                              ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                           TYPE: PRT
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
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Hanzel, David K.
Chen, Wensheng
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; OTHER INFORMATION:
US-09-864-761-47595
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Matches
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                                                                                                                                          NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Announce
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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CURRENT FILING DATE: 2001-05-23
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OTHER INFORMATION: MAP TO AC025863.2 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, OTHER INFORMATION: EXPRESSED IN FETAL LIVER,
                                                  TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                     LENGTH:
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APPLICATION NUMBER: US 09/774,203
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00667
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                                                                                                                                                                                                             APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                              FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
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                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
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Hanzel, David K.
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                                                                                                                                        Listing
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Pred. No.
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                                                                                                                                      Engine vers.
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 SIGNAL
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RESULT 11
US-09-970-088-11
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
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                                                                                                                                                                           Matches
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LENGTH: 124
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Best Local
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A. APPLICANT: Mannion, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/218,950 PRIOR FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.89
OTHER INFORMATION: EST_HUMAN HIT: BE958511.1, EVALUE 3.00e-40
OTHER INFORMATION: SWISSPROT HIT: Q50028, EVALUE 8.90e-01
                                                                                         107
                                                                                                                                1 SYDA 4
                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/206,201 FILING DATE: 2000-05-22
                                                                                      SYDA 110
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Pred. No. 1.5e+02;
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Pred. No. 1.3e+02;
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US-09-970-088-13
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US-09-970-088-12
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                                                                       Sequence 13, Application US/09970088 Patent No. US20020151489A1 GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: GRAVEREAUX, EDWIN G.
APPLICANT: SILVER, MARCY
APPLICANT: ISNER, JEFFREY M.
APPLICANT: YOON, YOUNG-SUP
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 140
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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                                    APPLICANT: GRAVEREAUX, EDWIN C. APPLICANT: SILVER, MARCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ISNER, JEFFREY M.
APPLICANT: YOON, YOUNG-SUP
TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 71417/55062
CURRENT APPLICATION NUMBER: US/09/970,088
CURRENT FILING DATE: 2001-10-02
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/237,171 PRIOR FILING DATE: 2000-10-02
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APPLICANT: YOON, YOUNG-SUP
TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS TO TREAT LYMPHATIC
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 71417/55062
CURRENT FAPLICATION NUMBER: US/09/970,088
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/237,171
PRIOR PILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 14
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SILVER, MARCY ISNER, JEFFREY M. YOON, YOUNG-SUP
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Pred. No. 1.6e+02;
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Pred. No. 1.6e+02;
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US-09-970-088-14
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SEQ ID NO 13
LENGTH: 140
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                               Sequence 306, Application US/09881752A Patent No. US20020115078A1
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SEQ ID NO 14
LENGTH: 140
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Best Local :
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                                       APPLICANT: Tomb, Jean-Francois
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020115078A1el Helicobacter Polypeptides
TITLE OF INVENTION: Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-970-088-13
                                                                                                                                            APPLICANT: Kleanthous, Harold APPLICANT: Al-Garawi, Amal APPLICANT: Miller, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ISNER, JEFFREY M.
APPLICANT: YOUN, YOUNG-SUP
TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS TO TREAT LYMPHATIC
TITLE OF INVENTION: DISORDERS
             TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
CURRENT APPLICATION NUMBER: US/09/881,752A
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CURRENT FILING DATE: 2001-10-02
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CURRENT APPLICATION NUMBER: US/09/970,088
CURRENT FILING DATE: 2001-10-02
CURRENT FILING DATE:
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APPLICANT: SILVER, MARCY
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                                                                                                                                                                                                                                                                                                                            135 SYDA 138
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4; Conservative
                                                                                                                                        Miller, Charles
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Pred. No.
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Pred. No. 1.6e+02;
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US-09-881-752A-306
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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Best Local S
Matches 4
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 3939
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 306
LENGTH: 144
                                                                        PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
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APPLICANT: Rank, David I
APPLICANT: Hanzel, David
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                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US01/00668 PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00665
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PRIOR FILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US01/00662 PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US01/00663 PRIOR FILING DATE: 2001-01-30
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nes 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-01-30
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Pred. No. 1.7
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RESULT 18
US-09-738-626-6309
US-09-738-626-6309, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
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Best Local Similarity
"---hes 4; Conserva
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; SEQ ID NO 4419
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SENCH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION UNMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 90/159162
PRIOR APPLICATION NUMBER: UP 00/159162
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OTHER INFORMATION:
OTHER INFORMATION:
US-09-864-761-39939
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APPLICANT: NAKAGAWA, SATOSHI
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                                                                                                                                                   119 SYDA 122
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
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N. EXPRESSED IN LUNG, SIGNAL = 1.9

N. EXPRESSED IN HEART, SIGNAL = 1.9

N. EXPRESSED IN HEART, SIGNAL = 1.9

N. EXPRESSED IN BRAIN, SIGNAL = 2.4

N. EXPRESSED IN HELA, SIGNAL = 2.4

N. EXPRESSED IN HELA, SIGNAL = 2.7

N. EXPRESSED IN HELA, SIGNAL = 2.7

N. EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

N. EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
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Pred. No. 2e+02;
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Pred. No. 1.9e+02;
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: U9/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN Ver. 3.0
SEQ ID NO 6309
SEQ ID NO 6309
                                                    ; ORGANISM: Corynebacterium glutamicum US-09-738-626-5341
                                                                                                                                                                                                                         APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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US-09-738-626-5341
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                                                                                                                                    PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 5341
Query Match
Best Local Similarity
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Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                 LENGTH: 219
TYPE: PRT
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OCHIAI, KEIKO
YOKOI, HARUHIKO
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SENOH, AKIHIRO
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YOKOI, HARUHIKO
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100.0%; ilarity 100.0%; Conservative 0

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Score 21; DB 9; Pred. No. 2.5e+02; Mismatches 0;

Length 219; Indels

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Gaps

B 8

109

SYDA 4 |||| SYDA 112

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APPLICANT: Dilkes, Brian x.

APPLICANT: Sun, Yuejin

TITLE OF INVENTION: Cell Cycle Nucleic Acids, Polypeptides and FILE REFERENCE: 1146

CURRENT APPLICATION NUMBER: US/09/993,308

CURRENT FILING DATE: 2001-11-06

PRIOR APPLICATION NUMBER: 60/246,349

PRIOR FILING DATE: 2000-11-07

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin version 3.1

SEQ ID NO 2

LENGTH: 256

TYPE: PRT

ORGANISM: Zea mays

US-09-993-308-2
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SEQ ID NO 958
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (7)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-958
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US-09-925-299-958
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Best Local Similarity
Matches 4; Conserv
                                                                      Matches
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Best Local Similarity
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gordon-Kamm, William J.
APPLICANT: Lowe, Keith S.
APPLICANT: Larkins, Brian A.
APPLICANT: Dilkes, Brian R.
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
138 SYDA 141
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                                  1 SYDA 4
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                                                                    Conservative
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                                                                                   100.0%;
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                                                                      0;
                                                                  Score 21; DB 9;
Pred. No. 2.9e+02;
Mismatches 0;
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                                                                                                    Length 256;
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                                                                    Indels
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                                                                    Gaps
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; LENGTH: 267
; TYPE: PRT
; ORGANISM: HOMO S
US-09-808-602-25
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Query Match
Best Local Similarity
Thes 4; Conserv
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                                                                                                                                                          SOFTWARE: PatentIn Ver. SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding
FILE REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
                                                                                                                                                                                                                                                                        APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
FILE REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
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                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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PRIOR FILING DATE: 2000-03-03
                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 114
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Mishra, Vishnu
Mezes, Peter S
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Shimkets, Richard A
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Mezes, Peter S
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Shimkets, Richard A
Herrman, John L
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                Conservative
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                               100.0%; Score 21; DB 9; 100.0%; Pred. No. 3.1e+02;
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Pred. No. 3.1e+02;
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                Mismatches
                                              Length 267;
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                Indels
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1 SYDA 4

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SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 3633
LENGTH: 271
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-3633
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CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 101
SEQ ID NO 101
LENGTH: 267
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US-09-738-626-3633
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US-09-808-602-101
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Best Local Similarity
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Patent No. US20020155115A1
                                                                                                                        PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DATE: 2000-12-18 PRIOR APPLICATION NUMBER: UF 99/377484 PRIOR FILING DATE: 1999-12-16 PRIOR APPLICATION NUMBER: UF 00/159162 PRIOR APPLICATION NUMBER: UF 00/159162 PRIOR FILING DATE: 2000-04-07 PRIOR FILING DATE: 2000-04-07
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richau
APPLICANT: Herrman, John L
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TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
FILE REFERENCE: 15966-697 CIP
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SENOH, AKIHIRO
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Mishra, Vishnu
Mezes, Peter S
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Shimkets, Richard A
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186 SYDA 189

1 SYDA 4

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; SEQUENCE DESCRIPTION: SEQ
US-09-939-980-462
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US-09-939-980-462
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    Matches
              Query Match
Best Local Similarity
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Best Local Similarity 100.
The Conservative
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 462:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 SYDA 34
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                                                                                                                                                                                                                     TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/936,165
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/939,980
FILING DATE: 27-Aug-2001
CLASSIFICATION: cUnknown> |
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ward, Judith 1
TITLE OF INVENTION: No. US20020082234Alel Prokaryotic Polynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: Fastbeg for Windows Version 2.0
                                                                                                                                                                                                                                                                                   NAME: Gimmi, Edward R
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: King of Prussia STATE: PA
                                                                                                                                                       LENGTH: 290 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 709 Swedeland
 100.0%; ilarity 100.0%; Conservative 0;
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Burnham, Martin
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                                                                            SEQ ID NO: 462:
Score 21; DE
Pred. No. 3.3
0; Mismatches
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DB 10;
. 3.3e+02;
ches 0;
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                              Length 290;
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Gaps
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0;
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; TYPE: PRT; ORGANISM: Corynebacterium glutamicum US-09-738-626-4308
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APPLICANT: Fernand
APPLICANT: Shimket
APPLICANT: Herrman
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Best Local Similarity
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LENGTH: 321
 Query Match
                                                                                         SEQ ID NO 4308
LENGTH: 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4308, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
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APPLICANT: MIZOGUCHI, HIROS
APPLICANT: ANDO, SEIKO
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PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
FILE REFERENCE: 15966-697 CIP.
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CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
                                                                                                                                              PRIOR APPLICATION NUMBER: JP 00/280988 PRIOR FILING DATE: 2000-08-03 NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                      FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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                                                                                                                             SOFTWARE: PatentIn ver. 3.0
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                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 SYDA 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vernet, Corine A
Fernandes, Elma
Shimkets, Richard A
                                                                                                                                                                                                                                                                                                                                                                                     YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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OCHIAI, KEIKO
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Mishra, Vishnu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herrman, John L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 21; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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 100.0%;
 Score 21;
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 DB 9;
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Length 332;
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Query Match
Best Local Similarity
""" (Conservation)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT ; ORGANISM: Corynebacterium glutamicum US-09-962-618-2
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US-09-815-242-10953
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                                NUMBER OF SEQ ID NO SOFTWARE: FastSEQ f SEQ ID NO 10953 LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-962-618-2
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LENGTH: 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09962618 Patent No. US20020103357A1
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APPLICANT:
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                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BATHE, Brigitte
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE msik GENE
FILE REFERENCE: 032301 WD 228
                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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SOFTWARE: PatentIn version 3.1
                                                                                                                    PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                      PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
ORGANISM: Haemophilus influenzae
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314 SYDA 317
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Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen, Kari L.
Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carr, Grant
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                                                                   for Windows Version 4.0
                                                                                                    2001-02-16
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Pred. No.
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); Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
                                                                                                                                                                                                             RESULT 32
US-09-738-626-4252
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US-09-815-242-10844
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                                                                                                                                                                      Sequence 4252, Application US/09738626 Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10844
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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Patent No. US20020061569A1
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Best Local Similarity
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR EILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
APPLICANT:
                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-3
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 343
TYPE: PRT
                                                                                                                                                                                                                                                                                           178 SYDA 181
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Local Similarity 100.0%; Pred. No. 3.
es 4; Conservative 0; Mismatches
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                                                                                                            MIZOGUCHI, HIROSHI
              YOKOI, HARUHIKO
TATEISHI, NAOKO
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Trawick, John D.
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Zyskind, Judith W.
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US-09-888-615-95

Sequence 95, Application US/09888615
Patent No. US20020064856A1
GENERAL INFORMATION:
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                                                                                         RESULT 34
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NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 4252
LENGTH: 345
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 105
                                                                                                                                                                                                                    Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                      Query Match
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Patent No. US20020155115A1
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APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115A1el Proteins and Nuclec Acids Encoding Same
FILE REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
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                                                                                                                                                                                                                                                                                                      LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
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Mezes, Peter S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Majumder, Kumud
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Shimkets, Richard A
                                                                                                                                                                                                                  100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vishnu
                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                 Score 21; DB 9;
Pred. No. 4e+02;
                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                      DB 9;
                                                                                                                                                                                                                                                 Length 352;
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RESULT 35
US-09-799-777-45
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 45, Application U Patent No. US20020091244A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE ON TOWN TION: OUTE PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                         INFORMATION FOR SEQ ID NO: 45: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 SYDA 245
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
                                                                                                                                                       APPLICATION NUMBER: US/09/002,485
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0459 US
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/799,777
FILING DATE: 06-Mar-2001
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS NUMBER OF SEQUENCES: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: PALO ALTO
STATE: CALIFORNIA
                     LENGTH: 359 amino acids TYPE: amino acid
STRANDEDNESS: single
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Corley, Neil C.
Guegler, Karl J.
Baugh, Mariah
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                                                                                                                       855-0555
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Pred. No.
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Query Match
Best Local Similarity
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                                                                                                                                                                                                 US-09-815-242-11378
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn ver. 3.0 SEQ ID NO 5241 LENGTH: 360
                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                  Sequence 11378, Application US/09815242 Patent No. US20020061569A1
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                    APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: JP 99/377484 PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                             APPLICANT:
                                                          APPLICANT:
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                              APPLICANT:
FITLE OF INVENTION:
              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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TATEISHI, NAOKO
SENOH, AKIHIRO
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CLONE: 1988911
                                                                                                   Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAYASHI, MIKII
OCHIAI, KEIKO
                                         Carr, Grant J.
Yamamoto, Robert T.
                                                                      Trawick, John D.
                                                                                          Wall, Daniel
                           Xu, H. Howard
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illarity 100.0%;
Conservative C
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            Identification
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Pred. No. 4.1e+02;
); Mismatches 0;
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Pred. No. 4.1e+02;
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              of Essential Genes
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                                                                                            ; ORGANISM: Corynebacterium glutamicum US-09-738-626-5738
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US-09-738-626-5738
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US-09-815-242-11378
                               Matches
                                                                 Query Match
                                                                                                                                                                   SEQ ID NO 5738
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Best Local Similarity 100.
Matches 4; Conservative
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 11378
LENGTH: 360
                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTMARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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CURRENT FILING DATE: 2001-03-21
                                                                                                                                                     ENGTH:
                                              Local Similarity
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1 SYDA 4
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                        4.
                                                                                                                                                   378
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TATEISHI, NAOKO
SENOH, AKIHIRO
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OCHIAI, KEIKO
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                              Conservative
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                                        100.0%;
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                                        Score 21; DB 9;
Pred. No. 4.3e+02;
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Pred. No. 4
                          Mismatches
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CURRENT APPLICATION NUMBER: US/09/971,536

CURRENT FILING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: U.S. NO. US20020159976A1 09/634,238

PRIOR APPLICATION NUMBER: U.S. NO. US20020159976A1 09/724,623

PRIOR APPLICATION NUMBER: U.S. NO. US20020159976A1 09/724,623

PRIOR FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: PCT/WZ01/00160

PRIOR FILING DATE: 2001-08-08

NUMBER OF SEQ ID NOS: 83

SOFTWARE: FASTSEQ for Windows Version 4.0

LENGTH: 416
                               TITLE OF INVENTION: Identification of ES
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION UNMBER: US/09/815,24
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-28
PRIOR FILING DATE: 2000-05-26
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Best Local Similarity
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APPLICANT:
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Patent No. US20020061569A1
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                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Reid, Julian
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Lactobacillus rhamnosus Polynucleotides, Polypeptides and Meth
TITLE OF INVENTION: Using Them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Lactobacillus rhamnosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 SYDA 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SYDA 4
APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                         Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                          Carr, Grant J.
                                                                                                                                                                                                                                                                                                                            Ohlsen, Kari L.
Zyskind, Judith W.
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                                                                                                                                                                                                                                                          Yamamoto, Robert T.
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O'Toole, Paul
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Pred. No.
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                                                                                                                                                                                                                   Essential Genes
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5696
LENGTH: 439
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5696
APPLICANT: Ohlsen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 5001-03-21
PRIOR APPLICATION UNDER: 500/191,078
PRIOR FILING DATE: 2001-03-21
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US-09-815-242-5045
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US-09-820-893-56
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
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LENGTH: 491
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 5045, Application US/09815242 Patent No. US20020061569A1
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Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 56, Application US/09820893 Patent No. US20020076705A1
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/531,119
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/102,895
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: 31 Human Secreted Proteins
FILE REFERENCE: PZ033P1
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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US-09-815-242-5045
                                                                                        ; ORGANISM: Klebsiella
US-09-815-242-11757
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                                                                                                                                               NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11757
LENGTH: 506
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5045
  Query Match 100.
Best Local Similarity 100
Matches 4; Conservative
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/206,848
PRIOR TILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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APPLICANT: Ohlsen, Kari L.
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2000-10-23
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Zyskind, Judith W.
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100.0%; Score 21; DB 10; 100.0%; Pred. No. 5.7e+02; O: Mismatches 0;
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                                       Length 506;
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Sequence 4, Application US/09824735
Patent NO. US20020095032A1
GENERAL INFORMATION:
APPLICANT: ZHJ, JIAN'KANG
APPLICANT: LIU, JIPING
APPLICANT: ISHITANI, MANABU
APPLICANT: HALFTER, URSULA
APPLICANT: KIM, CHEOL-SOO
TITLE OF INVENTION: PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS
FILE REFERENCE: 205645US20
CURRENT APPLICATION NUMBER: US/09/824,735
CURRENT FILING DATE: 2010-08-17
PRIOR APPLICATION NUMBER: US 60/824,735
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 4
LENGTH: 552
TYPE: PRT
US-09-824-735-4
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ITILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1909-03-12
NUMBER OF SEQ ID NO 477
SEQ ID NO 477
LENGTH: 549
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US-09-925-302-477
; Sequence 477, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
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US-09-824-735-4
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Best Local S
Matches 4
                                                      Query Match 100.0%; Score 21; DB 10; Best Local Similarity 100.0%; Pred. No. 6.2e+02; Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
LOCATION: (224)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KBY: SITE
LOCATION: (217)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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ORGANISM: Homo sapiens
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225 SYDA 228
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Local Similarity 100.0%; Pred. No. 6.1e+02;
nes 4; Conservative 0; Mismatches 0;
1 SYDA 4
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                                                                                           DB 10; Length 552;
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                                                        Indels
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Db 282 SYDA 285

Search completed: February 6, 2003, 11:39:44
Job time: 6.83333 secs

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Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
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                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                              Score
            21
21
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Match Length
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/cgn2_6/ptodata/1/paa/US084_COMB.pep:*
/cgn2_6/ptodata/1/paa/US086_COMB.pep:*
/cgn2_6/ptodata/1/paa/US086_COMB.pep:*
/cgn2_6/ptodata/1/paa/US086_COMB.pep:*
/cgn2_6/ptodata/1/paa/US089_COMB.pep:*
/cgn2_6/ptodata/1/paa/US089_COMB.pep:*
/cgn2_6/ptodata/1/paa/US090_COMB.pep:*
/cgn2_6/ptodata/1/paa/US091_COMB.pep:*
/cgn2_6/ptodata/1/paa/US092_COMB.pep:*
/cgn2_6/ptodata/1/paa/US093_COMB.pep:*
/cgn2_6/ptodata/1/paa/US093_COMB.pep:*
/cgn2_6/ptodata/1/paa/US093_COMB.pep:*
/cgn2_6/ptodata/1/paa/US095_COMB.pep:*
/cgn2_6/ptodata/1/paa/US095_COMB.pep:*
/cgn2_6/ptodata/1/paa/US095_COMB.pep:*
/cgn2_6/ptodata/1/paa/US095_COMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/paa/US07_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US099_COMB.pep:*
/cgn2_6/ptodata/1/paa/US100_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US102_COMB.pep:*
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    3 US-09-908-943A-178
7 US-60-275-251-178
US-08-310-912-126
12 US-09-867-852-126
12 PCT-US02-11643-95
PCT-US02-11643-307
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Sequence 178, App
Sequence 178, App
Sequence 126, App
Sequence 126, App
Sequence 95, App1
Sequence 307, App
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equence 529	equence 5244,	quence 5109,	equence 4949,	equence 4800,	equence 4799,	equence 4647,	equence 4532,	equence 4448,	equence 4385,	equence 4204,	equence 4149,	equence 4066,	equence 3971,	equence 3910,	equence 3758,	equence 3496,	equence 3306,	equence 3305,	equence 3188,	equence 3161,	equence 3160,	equence 2863,	equence 2862,	equence 2733,	equence 2579,	2398,	equence 2379,	equence 2132	equence 1988.	equence 1912	equence 1838, A	equence 1760, A	equence 1569. A	equence 1043, A	equence 817, Ap	equence 771, Ap	e 556, Ap	equence 55
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ALIGNMENTS

RESULT 1
US-09-908-943A-178

Sequence 178, Application US/09908943A

Sequence 178, Application US/09908943A

GENERAL INFORMATION:
APPLICANT: Yan, Riqiang
APPLICANT: Tomassell1, Alfredo G.
APPLICANT: Emmons, Thomas L.
APPLICANT: Blenkowski, Mike J.
APPLICANT: Blenkowski, Mike J.
APPLICANT: Blenkowski, Mike J.
APPLICANT: Heinrikson, Robert L.
TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
FILE REFERENCE: 29915/00281A.US1
CURRENT APPLICATION NUMBER: US/09/908,943A
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 05/219,795
PRIOR FILING DATE: 2000-07-19

PRIOR FILING DATE: 2000-07-19

NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 178
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide sequence
US-09-908-943A-178

Query Match
Best Local Similarity 100.0%; Pred. No. 4.2e+06;

Matches

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Conservative

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Mismatches

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Indels

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Gaps

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US-08-310-912-126
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CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 178
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 126, Application US/08310912 GENERAL INFORMATION:
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY FILE REFERENCE: 29915/00281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                              CURRENT APPLICATION NUMBER: US/08/310 017

ELLING DATE: CLASSITETC: US/08/310 017
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                         APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND
NUMBER OF SEQUENCES: 201
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ausubel, Frederick M. APPLICANT: Staskawicz, Brian J.
                                                                                                                                                                                                                                                                                                                    APPLICANT:
CLASSIFICATION: 800 RIOR APPLICATION NUMBER: 1
                                                                                                                                                                   COUNTRY: USA
ZIP: 02110-2904
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Heinrikson, Robert L.
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                                                                                                                                                                                                                            E: Fish & Richardson
225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                 Dahlbeck, Douglas
Katagiri, Fumiaki
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   US 08/227,360
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              Sequence 95. Application PC/TUS0211643 GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M. APPLICANT: Raitano, Arthur B.
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 126, Application US/0986
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
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Best Local
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 09/301,085
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND TITLE OF INVENTION: DETECTION METHODS FILE REFERENCE: 00786/254002
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INFORMATION FOR SEQ ID NO:
APPLICANT:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                     1 SYDA 4
                                                                                                                                                                                                                                                      Local Similarity
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Faris, Mary
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Katagiri, Fumiaki
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Pred. No. 4
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Pred. No. 4.2e+06;
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1.2e+06;
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APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 184P1EZ USEFUL IN TREATMENT AND

FILE REFERENCE: 51158-20067.40

CURRENT APPLICATION NUMBER: PCT/US02/11643

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR APPLICATION NUMBER: US 60/286,630

PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR FILING DATE: 2001-04-10

PRIOR FILING DATE: 2001-04-25

NUMBER OF SEQ ID NOS: 15017

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 307

LENGTH: 9

TYPE: DRT
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RESULT 7
PCT-US02-11643-552
Sequence 552, Application
GENERAL INFORMATION:
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; ORGANISM: Homo Sapiens
PCT-US02-11643-95
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 95
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR PILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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Morrison, Robert K.
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APPLICANT: MOTTISON, ROBERT K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/USC2/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 556
LENGTH: 9
TYPE: PRT
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; TYPE: PRT
; ORGANISM: Homo Sapiens
PCT-US02-11643-552
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 552
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Best Local :
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APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184PIEZ USEFUL IN TREATMENT AND DETECTION OF CANCER
TILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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Morrison, Robert K.
Ge, Wangmao
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Rubert, Rene S.
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Pred. No. 4.2e+06;
; Mismatches 0;
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RESULT 9

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APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Rubert, Rene S.
APPLICANT: Morrison, Karen J.
APPLICANT: Morrison, Robert K.
                                                                                                                                                    Matches
                                                                                                                                                                                                                             Query Match
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 771
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
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Rubert, Rene S.
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Morrison, Robert K.
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                                                                                                                                                Conservative
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                                                                                                                                        Score 21; DB 1;
Pred. No. 4.2e+06;
Mismatches 0;
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Pred. No. 4
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                                                                                                                                                                                                             Length 9;
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CT-US02-11643-1569
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; Sequence 1569, Application PC/TUS0211643
; GENERAL INFORMATION:
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PCT-US02-11643-1043
                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version ^{1}4.0 SEQ ID NO 1569
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PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1043
LENGTH: 9
        Matches
                                              Query Match
                                                                                                                                                                                                                  APPLICANT: JAKOBOVIES, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P122 USEFUL IN TREATMENT A
FILE REFERENCE: 51188-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
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APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT A
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
CURRENT FILING DATE: 2002-04-09
CURRENT FILING DATE: 2002-04-09
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APPLICANT:
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APPLICANT:
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                                                                                                           ORGANISM:
                                                                                                                              TYPE: PRT
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      Local Similarity tes 4; Conserv
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Morrison, Robert K.
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Rubert, Rene S.
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        Conservative
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                     Score 21; DB 1;
Pred. No. 4.2e+06;
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Pred. | No. 4
    Mismatches
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                                               PCT-US02-11643-1838
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1760
LENGTH: 9
TYPE: PRT
  Query Match
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APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT A
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT;
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60,286,630 PRIOR FILING DATE: 2001-04-25 NUMBER OF SEQ ID NOS: 15017
                                                                                           LENGTH: 9
TYPE: PRT
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                                                                   ORGANISM: Homo Sapiens
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Rubert, Rene S.
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Morrison, Robert K.
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100.0%; Score 21;
DB
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                                                       PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1988
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1912
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Matches 4; Conserv
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                                                                                                                                                           APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
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APPLICANT:
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
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TYPE: PRT
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ORGANISM: Homo Sapiens
                                        ENGTH:
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Morrison, Karen J.
Morrison, Robert K.
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Morrison, Robert K.
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Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9;
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RESULT 18
PCT-US02-11643-2379
Sequence 2379, Application PC/TUS0211643
GENERAL INFORMATION:
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Best Local Similarity
Thes 4; Conserve
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PCT~USO2-11643-2132
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITIED 184P1EZ USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Raitano, Arth
APPLICANT: Faris, Mary
APPLICANT: Rubert, Rene S
APPLICANT: Morrison, Kare
                                                                                                                   APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AFILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
CURRENT FILING DATE: 2002-04-09
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 2379
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APPLICANT:
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                FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                       Ge, Wangmao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ge, Wangmao
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Morrison, Robert K.
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Pred. No. 4.2e+06;
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hes 0;
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APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184PLE2| USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR ETLING DATE: 2001-04-10
PRIOR ETLING DATE: 2001-04-25
PRIOR ETLING DATE: 2001-04-25
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Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2398
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Best Local S
                                                            APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
ARPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT A
FILE REFERENCE: 51158-20067.40
CURRENT FILING DATE: 2002-04-09
CURRENT FILING DATE: 2002-04-09
CURRENT FILING DATE: 2002-04-09
CURRENT FILING DATE: 2002-04-09
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PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
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APPLICANT:
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Similarity 100.0%;
4; Conservative 0
                                                                                                                                                                                          Morrison, Karen J.
Morrison, Robert K.
Ge, Wangmao
                                                                                                                                                                                                                                                     Rubert, Rene S.
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Rubert, Rene S.
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Pred. No. 4.2
0; Mismatches
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Pred. No. 4.2e+06;
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                                                                                                                               TREATMENT AND DETECTION OF CANCER
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PCT-US02-11643-2862 ; Sequence 2862, Application PC/TUS0211643 ; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2579
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APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
TITLE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: POT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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          APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Challita-Eid, Pia M. APPLICANT: Raitano, Arthur B.
                                                                                                                                                                                                                                          APPLICANT: Challita-Eid, Pia M. APPLICANT: Raitano, Arthur B.
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TYPE: PRT
ORGANISM: Homo Sapiens
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APPLICATION NUMBER:
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                                                                                                                                                        Morrison, Karen J.
Morrison, Robert K.
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                                                                                                                                                                                                    Rubert, Rene S.
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Pred. No.
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20667.40
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FRSATSEQ for Windows Version 4.0
SEQ ID NO 2863
LENGTH: 9
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                                                                                                                                                                                                                                                             PCT-US02-11643-3160
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                                                                                                                                                                                                                                             Sequence 3160, Application PC/TUS0211643
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APPLICANT:
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APPLICANT:
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PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: MORTISON, Karen J.
APPLICANT: MORTISON, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
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Local Similarity 100.0%;
hes 4; Conservative 0
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Local Similarity 100.0%; Pred. No.
hes 4; Conservative 0; Mismatch
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                                                                                                                                         Rubert, Rene S.
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Pred. No. 4.2e+06;
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RESULT 26
PCT-US02-11643-3188
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CURRENT FILLING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3160
                                                                                 Sequence 3188, Application PC/TUS0211643
GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
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PCT-US02-11643-3161
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3161
LENGTH: 9
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                                    APPLICANT:
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-25
      APPLICANT:
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Best Local Similarity
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TYPE: PRT
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APPLICANT:
APPLICANT:
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APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Rubert, Rene S.
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo Sapiens
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                             Faris, Mary
Rubert, Rene S.
Morrison, Karen J.
Morrison, Robert K.
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Jakobovits, Aya
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Morrison, Robert K.
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                                                                                                                                                                                                                                                                                                          Score 21; DB 1;
Pred. No. 4.2e+06;
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Pred. No. 4.2e+06;
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PCT-US02-11643-3306

Sequence 3306, Application PC/TUS0211643

GENERAL INFORMATION:
APPLICANT: Challita-Eld, Pia M.
APPLICANT: Faitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PRO
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PRO
TITLE OF INVENTION: ENTITIED 184P1E2 USEFUL IN TREATM
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-25
INUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
INUMBER: OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
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PCT-US02-11643-3305
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PCT-US02-11643-3305
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             APPLICANT:
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Best Local Similarity
Matches 4; Conserva
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TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 9
TYPE: PRI

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Rubert, Rene S.
Morrison, Karen J.
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Morrison, Karen J.
Morrison, Robert K.
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Pred. No. 4.2e+06;
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Pred. No. 4.2e+06;
Mismatches 0;
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PCT-US02-11643-3758; Sequence 3758, Application PC/TUS0211643; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
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                                                                                                        RESULT 30
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Best Local (
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 18491E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-25
NUMBER OF SECOLID ACID: NO. 2017
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR PILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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  APPLICANT:
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TYPE: PRT
ORGANISM: Homo Sapiens
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Ge, Wangmao
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Raitano, Arthur B
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100.0%; F
tive 0;
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Pred. No. 4.2
D; Mismatches
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Query Match
Best Local Similarity
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LENGTH: 9
TYPE: PRT
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PRIOR FILING DATE: 2001-04-10
PRIOR PEPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3910
LENGTH: 9
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Best Local Similarity
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TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR PLING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
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Morrison, Robert K.
Ge, Wangmao
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Conservative C
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                                                                                            Score 21; DB 1;
Pred. No. 4.2e+06;
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RESULT 32 PCT-US02-11643-3971; Sequence 3971, Ap.

Application PC/TUS0211643

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CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4066
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APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Rubert, Rene S.
APPLICANT: Morrison, Karen J.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
                                                                              Matches
                                                                                                                  Query Match
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GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
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APPLICANT:
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 1849122 USEFUL IN TREATMENT AFILE REFERENCE: 51158-2067,40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR PILING DATE: 2001-04-10
PRIOR PRIOR DATE: 2001-04-25
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                                                                                                                                                                       ORGANISM: Homo Sapiens
                                                                                                                                                                                                 TYPE: PRT
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TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 9
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nilarity 100.0%;
Conservative 0
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                                                                                          Score 21;
Pred. No.
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Pred. No. 4.2e+06;
                                                                        Mismatches
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                                                                                          4.2e+06;
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Best Local Similarity
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PCT-US02-11643-4204
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; ORGANISM: Homo Sapiens
PCT-US02-11643-4149
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                                                                                                                                                                              NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4204
                                     Matches
                                                     Query Match
Best Local :
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PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version | 4.0
SEQ ID NO 4149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                       APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P122 USEFUL IN TREATMENT A
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
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APPLICANT:
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APPLICANT:
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APPLICANT:
                                                                                                                     ORGANISM: Homo Sapiens
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TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067-09
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Challita-Eid, Pia M. APPLICANT: Raitano, Arthur B.
                                                                                                                                               TYPE: PRT
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                                                                                                                                                             LENGTH: 9
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                                   Local Similarity les 4; Conserv
1 SYDA 4
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Morrison, Robert K.
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Faris, Mary
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Morrison, Robert K.
Ge, Wangmao
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Rubert, Rene
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                               Score 21; DB Pred. No. 4.2); Mismatches
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Pred. No. 4.2e+06;
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                                                4.2e+06;
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; ORGANISM: Homo Sapiens PCT-US02-11643-4448
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PCT-US02-11643-4385
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4385
LENGTH: 9
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APPLICANT: Challita-Eid, Pia M.
                                          Query Match
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      Matches
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184PLE2 USEFUL IN TREATMENT AND DETECTION OF CANCER
TITLE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR PILING DATE: 2001-04-10
PRIOR PILING DATE: 2001-04-15
NUMBER OF SEQ ID NOS: 15017
NUMBER OF SEQ ID NOS: 15017
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CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
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PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT /
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Faris, Mary
Rubert, Rene S.
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Morrison, Robert K.
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Rubert, Rene S.
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    Conservative
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Pred. No. 4.2e+06;
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Pred. No. 4.2e+0
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APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 184P122 USEFUL IN TREATMENT AND DETECTION OF CANCER

FILE REFERENCE: 51158-20067.40

CURRENT APPLICATION NUMBER: PCT/US02/11643

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR FILING DATE: 2001-04-10

PRIOR FILING DATE: 2001-04-17

PRIOR FILING DATE: 2001-04-17

PRIOR FILING DATE: 2001-04-25

NUMBER OF SEQ ID NOS: 15017

SEQ ID NO 4532

LENGTH: 9

TYPET
                                                                                                                                          APPLICANT: Morrison, Karen J.

APPLICANT: Morrison, Robert K.

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND

FILE REFERENCE: 51158-20067.40

CURRENT APPLICATION NUMBER: PCT/US02/11643

CURRENT APPLICATION NUMBER: DCT/US02/11643

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR APPLICATION NUMBER: US 60/286,630

PRIOR APPLICATION NUMBER: US 60/286,630
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; ORGANISM: Homo Sapiens
PCT-US02-11643-4647
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PCT-US02-11643-4532
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                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4647
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Best Local Similarity
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                                                                                                                              NUMBER OF SEQ ID NOS: 15017
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                                         LENGTH: 9
TYPE: PRT
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l Similarity 100.0%;
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Pred. No. 4.2e+06;
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; ORGANISM: Homo Sapiens PCT-US02-11643-4799
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APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Rubert, Rene S.
APPLICANT: Morrison, Karen J.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
                                            APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT A
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US-60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US-60,286,630
PRIOR APPLICATION NUMBER: US-60,286,630
PRIOR APPLICATION NUMBER: US-60,286,630
PRIOR FILING DATE: 2001-04-25
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SEQ ID NO 4800
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Best Local Similarity
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             NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
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Morrison, Robert K.
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100.0%; Pred. No.
tive 0; Mismatch
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hes 0;
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                                                                                                                                                                                                      DETECTION OF CANCER
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APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PRO
TITLE OF INVENTION: ENTITLED 184PLE2 USEFUL IN TREATM
FILE REFERENCE: 51158-20067.40

CURRENT APPLICATION NUMBER: PCT/US02/11643

CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/286,630

PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR FILING DATE: 2001-04-10

PRIOR FILING DATE: 2001-04-25

NUMBER: US 60,286,630
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Best Local S
Matches 4
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Best Local Similarity
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067-40
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR PILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEO ID NOS: 15017
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 SEQ ID NOS: FastSEQ for
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Morrison, Robert K.
                                                                                                                                                                                                                                                                                   Rubert, Rene S.
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Morrison, Robert K.
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Version 4.0
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Pred. No. 4.2e+06;
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Pred. No. 4.2e+06;
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SEQ ID NO 5109

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APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 184PLE2 USEFUL IN TREATMENT AND

FILE REFERENCE: 51158-20067.40

CURRENT APPLICATION NUMBER: PCT/USO2/11643

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR APPLICATION NUMBER: US 60/286,630

PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR FILING DATE: 2001-04-10

PRIOR FILING DATE: 201-04-25

NUMBER OF SEQ ID NOS: 15017

SEQ ID NO 5244

LENGTH: 9

TYPE: PRT
ORGANISM: Homo Sapiens
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PCT-US02-11643-5244
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APPLICANT: Challita Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Rubert, Rene S.
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Best Local 9
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Best Local :
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APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENVITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
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APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Rubert, Rene S.
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Morrison, Karen J.
Morrison, Robert K.
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Morrison, Karen J.
Morrison, Robert K.
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PRIOR FILLING DATE: 2001-04-25

NUMBER OF SEQ ID NOS: 15017

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5290

LENGTH: 9

TYDE: PRT

ORGANISM: Homo Sapiens
PCT-US02-11643-5290

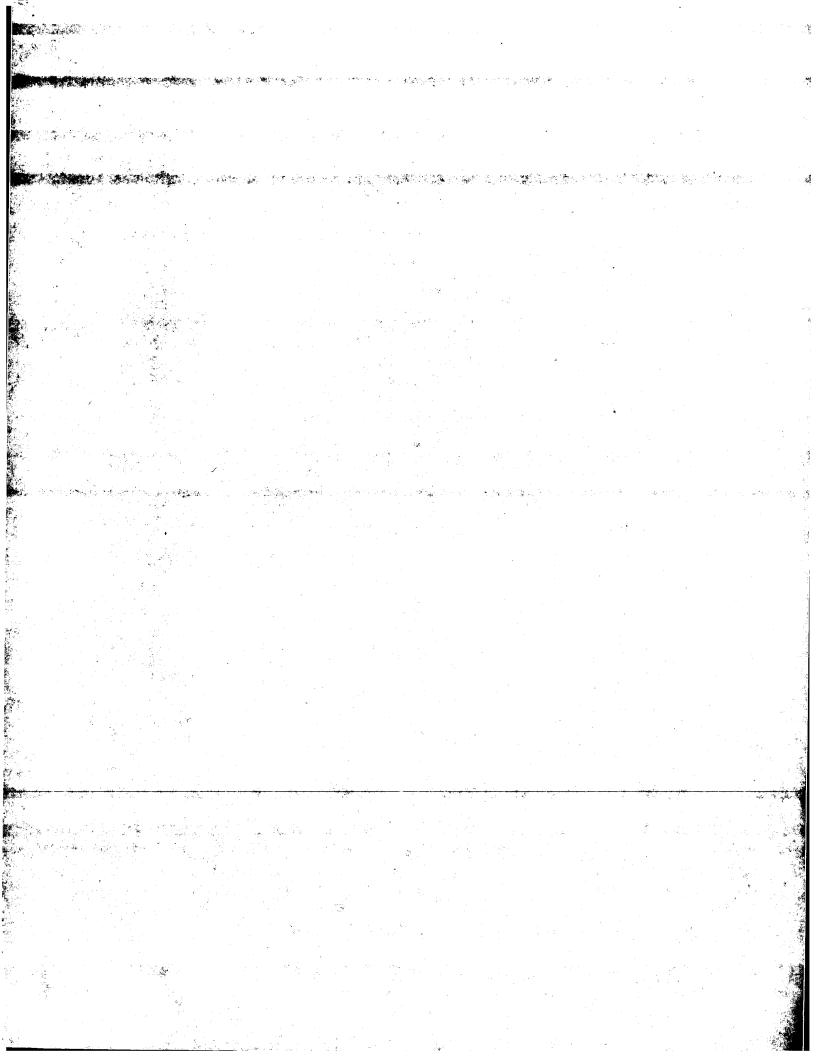
Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 SYDA 4

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Search completed: February 6, 2003, 11:37:33

Job time: 114.167 secs
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Minimum
Maximum
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23.165 Million cell updates/sec
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Listing first 45 summaries
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/cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
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     GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd
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US-10-203-138A-11128
US-10-203-138A-11208
US-10-276-781-1979
US-09-724-676-67729
US-09-513-999C-6382
US-09-513-999C-6627
US-09-724-676-67724
US-09-724-676-67728
US-09-724-676-67728
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US-09-724-676-67728
US-09-724-676A-67728
US-09-724-676A-67728
US-09-724-676A-67728
US-09-724-676A-67728
US-09-724-676A-67728
US-09-724-676A-67728
US-09-724-676A-67728
US-09-724-676A-67728
US-10-057-498-9695

PCT-US02-32727-25509

US-10-057-498-25509

US-09-950-084-7306

PCT-US02-32727-29763

US-09-724-676-67734

US-09-724-676-67734

PCT-US02-32727-24114

PCT-US02-32727-24114
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                      Sequence 292, App Sequence 1128, A Sequence 1179, Ap Sequence 67729, A Sequence 67724, A Sequence 67724, A Sequence 67726, A Sequence 5736, A Sequence 5736, A Sequence 25509, A Sequence 25509, A Sequence 25704, A Sequence 67734, A Sequence 67734, A Sequence 27114, A Sequence 24114, A Sequence 24114,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K. APPLICANT: Chen, Wensheng TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACI TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474 TITLE OF INVENTION: MOMBER: US/10/203,138A CURRENT APPLICATION NUMBER: US/10/203,138A CURRENT FILING DATE: 2002-08-02 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 26 May 2000 (26.05.00) US-10-203-138A-11128 ; Sequence 11128, Application US/10203138A ; GENERAL INFORMATION: ; ORGANISM: Homo sapien PCT-US02-41613-292 PRIOR APPLICATION NUMBER: 60/343,690 PRIOR FILING DATE: 2001-12-28 NUMBER OF SEQ ID NOS: 388 SOFTWARE: Patentin version 3.1 SEQ ID NO 292 Query Match Best Local Similarity Matches 4; Conserv Sequence 292, Application PC/TUS0241613 GENERAL INFORMATION: APPLICANT: Sun, Yongming APPLICANT: Liu, Chenghua TITLE OF INVENTION: Compositions and Methods Relating FILE REFERENCE: DEX-0370 CURRENT APPLICATION NUMBER: PCT/US02/41613 CURRENT FILING DATE: 2002-12-23 APPLICANT: diaDexus, Inc. APPLICANT: Macina, Roberto APPLICANT: Molecular Dynamics, Inc. LENGTH: 64 TYPE: PRT 18 SYDA 1 SYDA 4 100.0%; Score 21; DB 1; ilarity 100.0%; Pred. No. 1.5e+02; Conservative 0; Mismatches 0; Length 64; to Urinary Specific Genes an ACID 0; PROBES Gaps

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USEFUL

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(03.08.00)

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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 26 MAy 2000 (25.05.00)
PRIOR PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR FILING DATE: 21 September 2000 (21.09.00)
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                                                                                                                              NUMBER OF SEQ ID NOS: 15438
SOFTWARE: Molecular Dynamics Sequence Listing Engine LENGTH: 65
Type: ^~~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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LENGTH: 65
                                                                                                                                                                                                                               PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 30 June 2000 (30.06.00)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
FILE REFERENCE: PB 0004 WO 8
CURRENT APPLICATION NUMBER: US/10/203,138A
CURRENT FILING DATE: 2002-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Molecular Dynamics, Inc.
OTHER INFORMATION: EXPRESSED IN BT474,
                                              OTHER INFORMATION: MAP TO AP000044.1
                                                                      FEATURE:
                                                                                          ORGANISM: Homo sapiens
                                                                                                                    TYPE: PRT
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OTHER INFORMATION:
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FILING DATE: 03 October 2000 (03.10.00)
APPLICATION NUMBER: US 60/236,359
FILING DATE: 27 September 2000 (27.09.00)
APPLICATION NUMBER: US 60/234,687
FILING DATE: 21 September 2000 (21.09.00)
APPLICATION NUMBER: US 09/608,408
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FILING DATE: 03 August 2000 (03.0)
APPLICATION NUMBER: GB 24263.6
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Chen, Wensheng
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Rank, David R.
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Pred. No. 1.5e+02;
; Mismatches 0;
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SIGNAL
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FEATURE:

NAME/KEY: misc_feature

LOCATION: (14)...(14)

OTHER INFORMATION: Xaa can be any naturally occurring
US-09-724-676-67729
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; OTHER INFORMATION: SWISSPROT HIT: P22415, EVALUE 3.00e-17
US-10-203-138A-11208
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US-10-276-781-1979
                                                                                                                                                                                                                      FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 67729
LENGTH: 73
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al.
TITLE OF INVENTION: NOVel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-018 (785 contig)
CURRENT FILING DATE: 2002-11-18
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 2018
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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TYPE: PRT
                                                                                                                                 OTHER INFORMATION: Xaa can
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OTHER INFORMATION: EST_HUMAN HIT: AW937895.1, EVALUE 1.00e-16
    Local Similarity les 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            37 SYDA 40
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                Score 21;
Pred. No.
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Pred. No. 1.
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Pred, No. 1
   Mismatches
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                  1.7e+02;
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1.5e+02;
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SYDA SYDA

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US-09-724-676A-67729

Sequence 67729, Application US/09724676A

GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 67729
LENGTH: 73
RESULT 8
US-09-T13-999C-6627
; Sequence 6627, Application US/09513999C
; GENERAL INFORMATION:
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                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-513-999C-6382
                                                                                                                                                                                                                                                            SOFTWARE: Patent.pm
SEQ ID NO 6382
LENGTH: 75
TYPE: PRT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. FILE REFERENCE: 59.US2.REG CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Duclert, PAPPLICANT: Giordano,
                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 36681
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NAME/KEY: misc_feature
LOCATION: (11)..(12)
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                                                                                                 64 SYDA
                                                                                                                    1 SYDA 4
                                                                                                                                                               Local Similarity es 4; Conserv
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Pred. No.
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Pred. No. 1.7e+02;
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1.8e+02;
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                                                                                                                                                                                           US-09-724-676-67725
                                                                                   Sequence 67725, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
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SEQ ID NO 67724
LENGTH: 98
TYPE: PRT
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SEQ ID NO 6627
LENGTH: 77
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/00
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 67725
LENGTH: 98
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CURRENT FILING DATE: 2000-11-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa can
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Pred. No.
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RESULT 11
US-09-724-676-67726
Sequence 67726, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: VARIANTS of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
TEQUENCE: 05726
                                                                      Sequence 67728, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
LENGTH: 98
TYPE: COMPUSED OF SEQ ID NO 67728
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US-09-724-676-67728
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                                        ORGANISM: Homo sapiens
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OTHER INFORMATION: X
-09-724-676-67725
NAME/KEY: misc_feature LOCATION: (11)..(12)
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
FAATURE:
NAME/KEY: misc_feature
LOCATION: (11)...(12)
OTHER INFORMATION: Xaa can be any naturally occurring
                                  FEATURE:
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OTHER INFORMATION: Xaa
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RESULT 14
US-09-724-676A-67725
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LOCATION: (14)..(14);
OTHER INFORMATION: Xaa can be any naturally occurring amino US-09-724-676A-67724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 67724
LENGTH: 98
TYPE: PRT
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 67725
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                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
                                                                                                                                                                                                                                                                                            Sequence 67725, Application US/09724676A
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Best Local Similarity
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                                                        NAME/KEY: misc_feature LOCATION: (11)..(12)
OTHER INFORMATION: Xaa
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Best Local
 NAME/KEY: misc_feature LOCATION: (14)..(14) OTHER INFORMATION: Xaa
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
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NAME/KEY: misc_feature
LOCATION: (11)...(12)
OTHER INFORMATION: Xaa
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OTHER INFORMATION: X
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Pred. No. 2.4e+02;
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Pred.
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RESULT 16
US-09-724-676A-67728
US-09-724-676A-67728
Sequence 67728, Application US/09724676A

SEQUENCY INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 67728
LENGTH: 98
LENGTH: 98
LENGTH: PRT
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US-09-724-676A-67726
US-09-724-676A-67726
Sequence 67726, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
FILE OF INVENTION: Variants of alternative sp.
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 67726
LENGTH: 98
TYPE: PRT
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; NAME/KEY: misc_feature
; LOCATION: (14)...(14)
; OTHER INFORMATION: Xaa can be any naturally occurring amino US-09-724-676A-67726
                                                                 ; NAME/KEY: misc_feature ; LOCATION: (14) ...(14) ...(14) ...(15) OTHER INFORMATION: Xaa can be any naturally occurring amino acid US-09-724-676A-67728
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Query Match 100.0%; Best Local Similarity 100.0%; Matches 4; Conservative 0;
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Best Local Similarity
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OTHER_INFORMATION: Xaa can
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NAME/KEY: misc_feature
LOCATION: (11). (12)
OTHER INFORMATION: Xaa can
FEATURE:
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100.0%; Pred. NO. 2.4e+02;
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Pred. No. 2.4e+02;
Score 21; DB 5; 1
Pred. No. 2.4e+02;
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PCT-US02-32727-9695
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RESULT 19
PCT-US02-32727-25509
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GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
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Best Local :
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SEQ ID NO 9695
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CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514
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CURRENT FILING DATE: 2002-10-11
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514C1
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TYPE: PRT
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TYPE: PRT
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Barth, Brenda
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Bhatia, Ajay
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Jones, Robert
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llarity 100.0%;
Conservative 0
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US-09-950-084-7306 .

Sequence 7306, Application US/09950084 .

SERNERAL INFORMATION: .

APPLICANT: George H. Shimer, Jr. .

APPLICANT: George H. Miller .

APPLICANT: Roberta S. Hare .

APPLICANT: Karen J. Shaw .

ITILE OF INVENTION: Staphylococcus aureus Related Compositions and Methods .

FILE REFERENCE: 1034/10963US2
                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Propioni acnes US-10-057-498-25509
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PCT-US02-32727-25509
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SEQ ID NO 25509
LENGTH: 128
TYPE: PRT
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LENGTH: 128
TYPE: PRT
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APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
TITLE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
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APPLICANT: Skeiky,
APPLICANT: Persing,
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Ten, Shyian
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Bhatia, Ajay
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Carter, Darrick
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Wang, Siqing
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; ORGANISM: Propionibacterium acnes PCT-US02-32727-29763
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SEQ ID NO 29763
LENGTH: 157
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Best Local (
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Best Local Similarity
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APPLICANT: Barth, Brenda
APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
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PRIOR FILING DATE: 1998-03-06
PRIOR APPLICATION NUMBER: US 09/036,338
PRIOR FILING DATE: 1998-03-06
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PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/266,557
PRIOR FILING DATE: 1999-03-11
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CURRENT FILING DATE: 2001-09-10
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PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,555
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FILING DATE: 1999-03-11
APPLICATION NUMBER: US 09/037,934
FILING DATE: 1998-03-10
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APPLICATION NUMBER: US 09/266,542
FILING DATE: 1999-03-11
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ilarity 100.0%;
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Pred. No. 3.2e+02;
Mismatches 0;
               3.9e+02;
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US-09-724-676A-67734, Application US/09724676A; Sequence 67734, Application US/09724676A; GENERAL INFORMATION: APPLICANT: Compugen LTD: TITLE OF INVENTION: Variants of alternative splicing; FILE REFERENCE: 129181.4 Compugen
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 67734
LENGTH: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 67734
LENGTH: 159
TYPE: PRT
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Best Local Similarity
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                                                                                              APPLICANT:
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APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
APPLICANT: Bhatia, Ajay
APPLICANT: Maisonneuve, Jean
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                                                                                APPLICANT:
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Jen, Shyian
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Maisonneuve, Jean Francois
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                             Jones, Robert
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Brenda
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Pred. No.
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Pred. No. 4e+02;
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; ORGANISM: Propion1 acnes US-10-057-498-24114
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                                                                          NUMBER OF SEQ I
SEQ ID NO 24114
LENGTH: 166
TYPE: PRT
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Best Local S
Matches 4
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APPLICANT: Micham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
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LENGTH: 166
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Best Local Similarity
Query Match
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PRIOR FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/310,385
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 60/379,866
PRIOR FILING DATE: 2002-05-10
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TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO THE DAPTOMYCIN
TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER
FILE REFERENCE: CUB-12 PCT CIP
CURRENT APPLICATION NUMBER: PCT/US02/24310
CURRENT FILING DATE: 2002-10-25
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CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
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TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
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ilarity 100.0%;
Conservative 0
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Pred. No. 4.2e+02;
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Length 166;
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RESULT 30
US-09-724-676-67730
; Sequence 67730, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
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US-09-134-000C-6245
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Sequence 6245, Application US/09134000C
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS
FILE REFERENCE: 032796-032
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PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6245
LENGTH: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6245, Application US/09134000C
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
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Matches 4; Conserv
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SOFTWARE: PatentIn version 3.1
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TYPE: PRT
ORGANISM: Enterococcus faecalis
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tive 0;
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Pred. No. 4.5e+02;
; Mismatches 0;
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US-09-724-676-67732
; Sequence 67732, Appl:
; GENERAL INFORMATION:
RESULT 33
US-09-724-676-67733
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                                                                                                                                                                             ; ORGANISM: Homo sapiens US-09-724-676-67732
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                                                                                                                                                                                                             APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724;676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
LENGTH: 184
TYPE: PRT
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                                                                                                                                 Best
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SEQ ID NO 67731
LENGTH: 184
                                                                                                                       Matches
                                                                                                                                                    Query Match
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Best Local Similarity
Matches 4; Conserv
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SCETMANDED: Date: 10.05: 97222
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Best Local S
Matches 4
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 67730
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                                                             140 SYDA 143
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                                                                                                                                    Local Similarity
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Pred. No. 4.6e+02;
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Pred. No. 4.6e+02;
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Pred! No. 4.6e+02;
                                                                                                                   Mismatches
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RESULT 34

US-09-724-676A-67730

Sequence 67730, Application US/09724676A

SEMERAL INFORMATION:
APPLICANT: Compugen LTD
TILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT APPLICATION NUMBER: US/09/724,676A

UNMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 67730
LENGTH: 184
TYPE: PRT
                                                                                                                           GENERAL INFORMATION:

APPLICANT: Compugen LTD:

TITLE OF INVENTION: Variants of alternative splicing:

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 67731

LENGTH: 184

TYPE: PAT

ORGANISM: Homo sapiens

US-09-724-676A-67731
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US-09-724-676A-67731
; Sequence 67731, Application US/09724676A
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; ORGANISM: Homo sapiens
US-09-724-676-67733
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 67733
LENGTH: 184
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Local Similarity 100.0%;
nes 4; Conservative 0;
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                                                      100.0%; ilarity 100.0%; Conservative 0
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                                                  Score 21; DB 5; I
Pred. No. 4.6e+02;
; Mismatches 0;
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Pred. No. 4.6e+02;
; Mismatches 0;
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Pred. No. 4.6e+02;
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp.
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 67733
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-67733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 67732, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 67732
TENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-67732
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Best Local Similarity
Thehes 4; Conservi
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US-09-724-676A-67733
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US-09-724-676A-67732
                                                                                                                                                                                                                                                           Sequence 2328, Application US/10218140 GENERAL INFORMATION:
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Best Local :
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                              PRIOR APPLICATION NUMBER: 09/540,763
PRIOR ETILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/127,728
PRIOR ETILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/127,636
                                                                                                                                                                APPLICANT: Shinkets, Richard A.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 15966-543 CON
                                                                                                                           CURRENT APPLICATION NUMBER: US/10/218,140
CURRENT FILING DATE: 2002-08-12
                                                                                                                                                                                                                      APPLICANT: Leach, Martin D. APPLICANT: Shimkets, Richa
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               1999-04-02
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Pred. No. 4.6e+0;
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ches 0;
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; ORGANISM: Propioni acnes
US-10-057-498-16492
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US-10-057-498-16492
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; ORGANISM: Propioni acnes
PCT-US02-32727-16492
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PCT-US02-32727-16492
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Best Local Similarity
"~+~hes 4; Conserv?
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                                                                                                                         Sequence 16492, Application US/10057498
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Sketky, Vasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
                            CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 16492
LENGTH: 206
TYPE: PRT
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SEQ ID NO 16492
LENGTH: 206
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GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
APPLICANT: Bhatia, Ajay
APPLICANT: Maisonneuve, Jean Francois
APPLICANT: Zhang, Yanni
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NUMBER OF SEQ ID NOS: 6322
SOFTWARE: CUraNator Version 1.0
SEQ ID NO 2328
LENGTH: 199
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Douglass, John TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes FILE REFERENCE: 210121.514C1 CURRENT APPLICATION NUMBER: PCT/US02/32727 CURRENT FILING DATE: 2002-10-11
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APPLICANT:
APPLICANT:
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Ten, Shyian
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Barth, Brenda
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Pred. No. 5
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s 0;
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RESULT 43
US-09-724-676-97153
; Sequence 97153, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
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SOFTWARE: Patentin version
SEQ ID NO 3952
LENGTH: 213
TYPE: PRT
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Best Local :
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SEQ ID NO 3952
LENGTH: 213
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APPLICANT: LYNN DOUGETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS
FILE REFERENCE: 032796-032
CURRENT APPLICATION UMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
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Matches 4; Conserv
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PRIOR FILING DATE: 1997-08-15
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ORGANISM: Enterococcus
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RESULT 44
US-09-724-676A-97153
US-09-724-676A-97153, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
FILE REFERENCE: 129181.4 Compugen
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US-09-724-676-97142
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; ORGANISM: Homo sapiens
US-09-724-676-97142
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                                                                                                                                                                                                   APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 97142
TYPE: DATE: 231
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 97153
LENGTH: 224
TYPE: PRT
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 97153
LENGTH: 224
TYPE: PRT
                                                                     Query Match 100.0%; Score 21; DB 5; IBest Local Similarity 100.0%; Pred. No. 5.9e+02; Matches 4; Conservative 0; Mismatches 0;
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2: pir2:*
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h Sim 4;	ical protein s: Nostoc sp. Nostoc sp. s 14-Dec-2001 ion: AB1896 ion: AB1896 , T.; Nakamu i, N.; Shimp 8, 205-213, Complete Gen nce number: nce number: preliminar; preliminar; le type: DNA es: 1-53 <ku as10716<="" cs:="" mental="" references:="" sourc="" td=""><td>0-0 5</td><td>V-D-J Mus mu Mus mu Mus mu H15 n: pH15 n: pH25 d. 178 d. 178 olecula e numbe n: pH15 type: : 1-15 ntal sc : inmur</td><td></td><td>222222222222222222222222222222222222222</td></ku>	0-0 5	V-D-J Mus mu Mus mu Mus mu H15 n: pH15 n: pH25 d. 178 d. 178 olecula e numbe n: pH15 type: : 1-15 ntal sc : inmur		222222222222222222222222222222222222222
Similarity 4; Conser	ostoc sp. strain oc sp. strain oc sp. strain ec-2001 #sequ AB1896 ; Nakamura, Y 1: Shimpo, S. 2005-213, 2001 plete Genomic number: AB180 AB1896 elimlary ype: DNA 1-53 <kur> rences: GB:BA al source: st</kur>	Similarity 4; Conser A 4 1 1	-D-J region (wus musculus (hun 1994 #seque PH1582 D.A.; Campos-T 178, 317-329. ecular charact number: PH1580 PH1582 ype: DNA 1-15 <lev> al source: bon immunoglobulin</lev>		1100 000.000 000.0000 000.0000 000000000
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ore 21; DB ed. No. 98; Mismatches	- Nostoc sp. (strain PC. synonym of Anabaena sp. 14-Dec-2001 #text_change Kuritz, T.; Sasamoto, S; Takazawa, M.; Yamada, he Filamentous Nitrogen-85; PMID:11759840	ore 21; DB ed. NO. 25; Mismatches	5) - mouse 2-Jun-1994 2r, P. ansgene-in 3; PMID:831	MENTS	
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                                                                                               RESULT
T14992
                                                                                                                                                                                                                                                                                                                                                                              A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Sinoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1788
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A; Residues: 1-80 <GLA>
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Dominguez-Bernal, G.; Duchaud, E.; Durand,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision
C;Accession: AC1188
                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 294, 849-852,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B. subtilis YaaL protein homolog lin2849 [imported] - Listeria innocua (strain
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A; Residues: 1-67 < OKI>
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                                                                                                                                                                                                                                                                                                        Cross-references: GB:AL592022; PIDN:CAC98075.1; Experimental source: strain Clip11262
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Best Local
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Okinaka, R.T.; Cloud, K.; Hampton,
Bacteriol. 181, 6509-6515, 1999
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   Immun.
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Pred. No. 1.5e+02;
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           G.F.; Blattner,
                                     #text_change
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jurget, O.;
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Fsihi, H.
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DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7

A:Pafarence number: A99629; MUID:21156231; PMID:11258796
                                                                      A; Molecule type: DNA
A; Residues: 1-84 <HAY>
                                                                                                                                                                                                                                                                         R; Hayashi, T.; Makino, K.; Ohnishi, M.; gasawara, N.; Yasunaga, T.; Kuhara, S.;
                                                                                                                                                                                                                                                                                                                                                         hypothetical protein ECs1438 [imported] - Escherichia coli (strain O157:H7, C;Daecies: Escherichia coli (c;Daecies: 18-Jul-2001 #text_change 18-Ju
A;Cross-references: GB:BA000007; PIDN:BAB34861.1; PID:g13360902; A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simces, N.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;A;Ccession: AD1412
                                                                                                                               A; Status: preliminary
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A; Residues: 1-81 <GLA>
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C; Date: 27-Nov-2001
C; Accession: AD1412
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A;Genome:
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A; Residues: 1-81 <LIN>
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Best Local S
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Shiba, T.; Hattori,
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tian, K.D.;
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Voss, H.; Wehla
                                                                                                                                                                                                                                                                                                                                                                                                                        substrain
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Fsihi,
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Score

21;

DB 2;

Length

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A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: B8566 A;Status: preliminary
conserved hypothetical protein STY1199 [imported] - Salmonella e C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AB0638
                                                                                                                                                                                                                                                                                                                                                                 C;Accession: A64849
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; E
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A64849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein yceP [imported] - Escherichia C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001
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                                                                                                                                                                                                                                                                                          A; Experimental
                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
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                                                                              AB0638
                                                                                           RESULT 10
                                                                                                                                                                                                                                                              A; Gene:
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                                                                                                                                                                                                                                                                                                                                                     A; Status: nucleic acid sequence not
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Best Local
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Pred. No. 1.6e+02;
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Mismatches
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                  Mismatches
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hes 0;
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                 09-Nov-2001
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K.; Af
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A; Note:
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Query Match
Best Local Similarity
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RESULT 12
T31168
                                                                                                                                                         R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic
                                                                                                                                                                                                                                    hypothetical protein 392 - Sphingomonas aromaticivorans plasmid C;Species: Sphingomonas aromaticivorans C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Comment: This neuropeptide controls ecdysis.
C;Cupperfamily: eclosion hormone
F;1-26/Domain: signal sequence #status predicted <SIG>F;27-88/Product: eclosion hormone #status predicted <EV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 182, 514-519, 1992
A; Title: Nucleotide sequence of cDNA for the eclosion hormone A; Reference number: JS0644; MUID:92134263; PMID:1370883
A; Accession: JS0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Bombyx mori (silkworm)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jul-2000
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica s A;Reference number: AB0502; PMID:11677608
                                                        A; MOIECULE type: DNA
A; Residues: 1-95 < RO
                                                                                                                                    A; Description: Complete sequence A; Reference number: Z20992
                                                                                                                                                                                                                   C; Accession: T31168
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A; Residues: 1-88 < KAM>
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A; Residues: 1-85 < PAR>
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                                     A; Cross-references: EMBL: AF079317;
                                                                                             A; Status: preliminary; translated
                                                                                                                      A; Accession: T31168
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Best Local S
Matches 4
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                    Genetics:
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plasmid pNL1
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                                                            <ROM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No.
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Pred. No.
                                       NID:g3378261; PID:g3378309; PIDN:AAD03892.1
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                                                                                               GB/EMBL/DDBJ
                                                                                                                                                           kb catabolic
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1.7e+02;
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                                                                                                                                                                                                 S.J.; Sisk, E.C.; Sensen,
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Score Pred.

21; No.

DB 2; 1.9e+02;

Length

95

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RESULT 15
H84370
hypothetical protein Vng2202h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: H84370
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; (submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati A;Reference number: Z20992
A;Rocession: T31207
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein 680 - Sphingomonas aromaticivorans plasmid pNL1 C;Species: Sphingomonas aromaticivorans C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-F C;Accession: T31207 R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.I. Sisk F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: sequence extracted from NCBI backbone (NCBIN:113308, NCBIP:113309) C; Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology C; Keywords: 2Fe-2S; electron transfer; iron-sulfur protein; metalloprotein F; 25-79/Domain: ferredoxin [2Fe-2S] homology F; 40,45,48,78/Binding site: 2Fe-2S cluster (Cys) (covalent) #status prediction of the protein pr
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A;Experimental source: PCC 7002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-97 <LEO>
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J. Gen. Microbiol. 138, 1613-1621, 1992
A; Title: An iron stress operon involved in
A; Reference number: A47673; MUID:92407507;
A; Accession: C47673
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C;Species: Synechococcus sp.
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
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tes 4; Conserv
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100.0%; Pred. No. 2e+
tive 0; Mismatches
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Pred. No. 1.9e+02;
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R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evrolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: D97729
        A; Molecule type: DNA
A; Residues: 1-115 <KUR>
A; Cross-references: GB:
                                                                                                                                                                            hypothetical protein RC0236 [imported] - Rickettsia conorii (strain Malish C;Species: Rickettsia conorii C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001 C;Accession: D97729
                                                                 A; Status: preliminary
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A; Genome: plasmid
A; Note: plasmid M
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, Cl.M.
Science 286, 1571-1577, 1999
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A; Residues: 1-113 <WHI>
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A;Residues: 1-106 <STO>
A;Cross_references: GB:AE004437; NID:g10581619; PIDN:AAG20332.1; GSPDB:GN00138
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Proc. Natl. Acad. Sci. U.S.A. 97, 12176;12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.;
A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483; PMID:11016950
A; Accession: H84370
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Best Local
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GB:AE006914; PIDN:AAL02774.1; PID:g15619290; GSPDB:GN00173
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Pred. No.
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; Maddocks, D.(
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.G.; Ja
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SYDA 4

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A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Reterence : H95968
A;Reterence : H95968
A;Recession: H95968
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T23550
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H95968
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A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, A;Authors: Kahn, D.; Kahn, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number; A96039; MUID:21368234; PMID:11474104
                                                                                           A; Map position:
A; Introns: 25/3
                                                                                                                            A; Gene: CESP: K09G1.2
                                                                                                                                               A; Experimental source: C; Genetics:
                                                                                                                                                                             A;Cross-references: EMBL:Z81101; PIDN:CAB03198.1; GSPDB:GN00023;
                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-127 <WIL>
                                                                                                                                                                                                                                                   A; Reference number: A; Accession: T23550
                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, A; Reference number: Z19758
                                                                                                                                                                                                                                                                                                             R; Lloyd,
                                                                                                                                                                                                                                                                                                                        hypothetical protein K09G1.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #t.C;Accession: T23550
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A; Residues: 1-121 <KUR>
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C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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                                                                      Caenorhabditis elegans hypothetical protein K09G1.2
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Pred. No. 2.6
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2.6e+02;
hes 0;
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D.H.; Wong, K
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N.A.; Fisher, R.F.
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RESULT 20
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S77545
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C; Superf
C;Accession: C89791
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; S
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A;TItle: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C90733
                                                     C; Species: Staphylococcus aureus C; Date: 10-May-2001 #sequence_revision
                                                                                   hypothetical protein [imported] - Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: S77545
R;Kaneko, T.; Sato, S.; Kotani, O, K.; Okumura, S.; Shimpo, S.;
DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
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gasawara, N.; Yasunaga, T.; Kuhara, S.;
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
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A; Residues: 1-129 <KAN>
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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A; Residues: 1-128 <HAY>
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    Synechocystis sp.

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Shiba, T.; Hattori,
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ttori, M.; Shinagawa,
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     ; Cui, L.;
Sekimizu,
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A;Gene:
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A; Title: Genome sequence of enterohemorrhagic Escherichia A; Reference number: A85480; MUID:21074935; PMID:11206551 A; Raccession: E85583

A; Status: preliminary A; Molecule type: Nature 111.
                                                                                                                                                                                                                                                                                                                                                            phage related SSB-like protein [imported] - Clostridium acetobutylicum C;Specles: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 17-May-2002 C;Accession: G97136 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gib: Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
                                                                                          A; Experimental source: C; Genetics:
                                                                                                           A;Cross-references: GB:AE001437; PIDN:AAK79882.1; A;Experimental source: Clostridium acetobutylicum
                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-133 < KUR>
                                                                                                                                                                                                                                                              A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97136
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C;Superfamily: phage lambda minor tail protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable tail component of prophage CP-933K Z0973 [imported] -
C; Species: Escherichia coli
;Superfamily: bacterial single-stranded DNA-binding protein; single-stranded DNA-bindin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene:
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A; Residues: 1-130 < KUR>
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                                                                                                              PID:g15024899; GSPDB:GN00168
ATCC824
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uncharacterized conserved protein CAC2767<sub>l</sub> [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14<sup>L</sup>Sep-2001 #text_change 14-Sep-2001 C;Accession: D97240
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
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                                                                                                  D97240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein W07G1.4 - Caenorha C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision
                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                 A; Map position:
                                                                                                                                                                                                                                                                                                              A; Gene: CESP:W07G1.4
                                                                                                                                                                                                                                                                                                                                              A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:282076; NID:e1247330; PIDN:CAB04936.1; GSPDB:GN00020; CESP:W
                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-133 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: T26268
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T26268
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T35218
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A; Residues: 1-133 <SEE>
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R;Seeger, K.J.; Harr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library,
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Library, September 1998
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                                                                                                                                                                                                                   Score 121; DB
Pred. No. 2.7
); Mismatches
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Pred No. 2.7e+02;
Pred No. 2.7e+02;
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Pred: No. 2.7e+02;
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Markarova,
Smith, D.R.
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J. Bacteriol. 183, 4823-4838, ZUVI
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing bacula; Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D97240
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-13 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK80711.1; PID:g15025804; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thon R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraseam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: B87162
                                                                          C; Superfamily: in C; Keywords: T-cel F; 32-112/Domain:
                                                                                                                                                                                                                                                                                                                      rearranged T-cell receptor delta-chain/ Vdelta5.2-Ddeltas-Jdelta1 - C;Species: Sus scrofa domestica (domestic pig) C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-
                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-135 < YAN>
                                                                                                                                                                                    C;Accession: I46643
R;Yang, Y.G.: Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, J. Immunol. 155, 1981-1993, 1995
J. Immunol. 155, 1981-1993, 1995
A;Title: Diversity of T cell receptor delta-chain cDNA in A;Reference number: I46623; MUID:95363165; PMID:7636249
A;Accession: I46643
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-134 <STO>
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                                                                                                               A;Cross-references: GB:D49584; NID:g1041170; PIDN:BAA08528.1; PID:g1041171
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                ;Superfamily: immunoglobulin V region; ;Keywords: T-cell receptor
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Pred. No.
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Pred. No.
Score 21; DB 2; Pred. No. 2.8e+02; Mismatches 0;
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2.7e+02;
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A; Map position:
C; Superfamily: 1
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A; Reference number: AB2577; PMID:11743193
A; Accession: AE2644
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                                                                                                                                                                                                                                                                                                                                                                                                                                      flagellar basal-body rod protein [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: circular chromosome C; Superfamily: rod protein flgC
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A;Accession: E97426
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A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
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A; Residues: 1-139 < KUR>
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A;Residues: 1-139 <KUR>
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protein HI0589 -

Haemophilus influenzae (strain

Rd KW20)

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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A; Aluthors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987; PMID:9634230

A; Reference number: A70500; MUID:98295987; PMID:9634230

A; Status; preliminary; nucleic acid sequence not shown; translation not shown
                                                                    R;Moon, A.L.; Janmey, P.A.; Louie, K.A.; Drubin, D.G. J. Cell Biol. 120, 421-435, 1993
A;Title: Cofilin is an essential component of the yeast A;Reference number: A44397; MUID:93132073; PMID:8421056
                                                                                                                                                                 N;Alternate names: protein LO595; protein YLLO50c
C;Species: Saccharomyces cerevisiae
C;Date: 31-Dec-1993 #sequence_revision 27-Jun-1994 #text_change 21-Jul-2000
C;Accession: A44397; B44397; JN0529; S64802; S50970; S31309; S36087
A;Reference number: A44397;
A;Accession: A44397
A;Molecule type: DNA
A;Residues: 1-143 <MOO>
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A;Residues: 1-139 <COL>
A;Cross-references: GB:Z83860; GB:AL123456; NID:g3261681; PIDN:CAB06158.1; PID:e290748;
A;Experimental source: strain H37Rv
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C;Accession: F70661
C;Accession: F70661
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable lipoprotein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter
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A; Starus: 7:1-1-1
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A; Residues: 1-139 <TIGR>
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Best Local
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Escherichia coli sigma-E factor regulatory protein
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A; Gene: sod1
C; Superfamily:
C; Keywords: met
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R; Dennis, P.P.; Shimmin, L.C.
Microbiol. Mol. Biol. Rev. 61, 90-104, 1997
A; Title: Evolutionary divergence and salinity-mediated A; Reference number: Z22865; MUID:97257269; PMID:9106366
A; Accession: T44916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        superoxide dismutase (EC 1.15.1.1) (Fe) [similarity] - Haloferax mediterranei (fragme
C;Species: Haloferax mediterranei
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 24-Oct-2000
                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-144 <DEN>
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C; Superfami
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A;Residues: 'MWGKKFIRSQENVKFLCS',6-143 <WEW>
A;Cross-references: EMBL:Z47973; NID:g642313; PIDN:CAA88007.1;
C;Comment: Cofilin reversibly regulates actin polymerization and the second 
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submitted to the EMBL Data Library, January 1995
A;Description: Sequence of a 37 kb DNA fragment from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 12L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 124, 115-120, 1993
A;Title: Isolation of a yeast essential gene, COF1, that encodes a homologue of mamma A;Reference number: JN0529; MUID:93178959; PMID:8440472
A;Accession: JN0529
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A; Residues: 1-143 <WED>
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A; Residues: 1-143 <IID>
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       Query Match
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metalloprotein;
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n; oxidoreductase
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Pred No. 2.9e+02;
Pred No. 0;
       Score 21;
Pred. No.
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3e+02;
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Conservative

0,

Mismatches

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Gaps

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rearranged T-cell receptor delta-chain/Vdelta5.1-Ddeltas-Jdelta1 - pig (fragment) C;Species: Sus scrofa domestica (domestic pig) C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999 C;Accession: I46642
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A;Molecule type: DNA
A;Residues: 1-144 <KUR>
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A; Title: Genome Sequence and Comparative Analysis of the A; Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, J. Immunol. 155, 1981-1993, 1995
A;Title: Diversity of T cell receptor delta-chain cDNA in A;Reference number: 146623; MUID:95363165; PMID:7636249
A;Accession: I46642
A;Status: preliminary; translated from GB/EMBL/DDBJ
C;Accession: A64662
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; Mcison, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey Nature 388, 539-547, 1997
                                                                                             ATP synthase F0, subunit b' - Helicobacter pylori (strain 26695) C;Species: Helicobacter pylori C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A96900; A; Accession: H97356
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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A; Residues: 1-144 < YAN>
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A64662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: CAC3723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32-112/Domain: immunoglobulin homology <IMM>
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3e+02;
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Best Local
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Local

Similarity 4; Conserv

100.0%; llarity 100.0%; Conservative 0

0,

Mismatches

0

Indels

0

Gaps

0,

Score 21; Pred. No.

3e+02;

DB 2;

Length 145;

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C;Accession: A71856

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G. Nature 397, 176-180, 1999

Nature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric A;Reference number: A71800; MUID:99120557; PMID:9923682

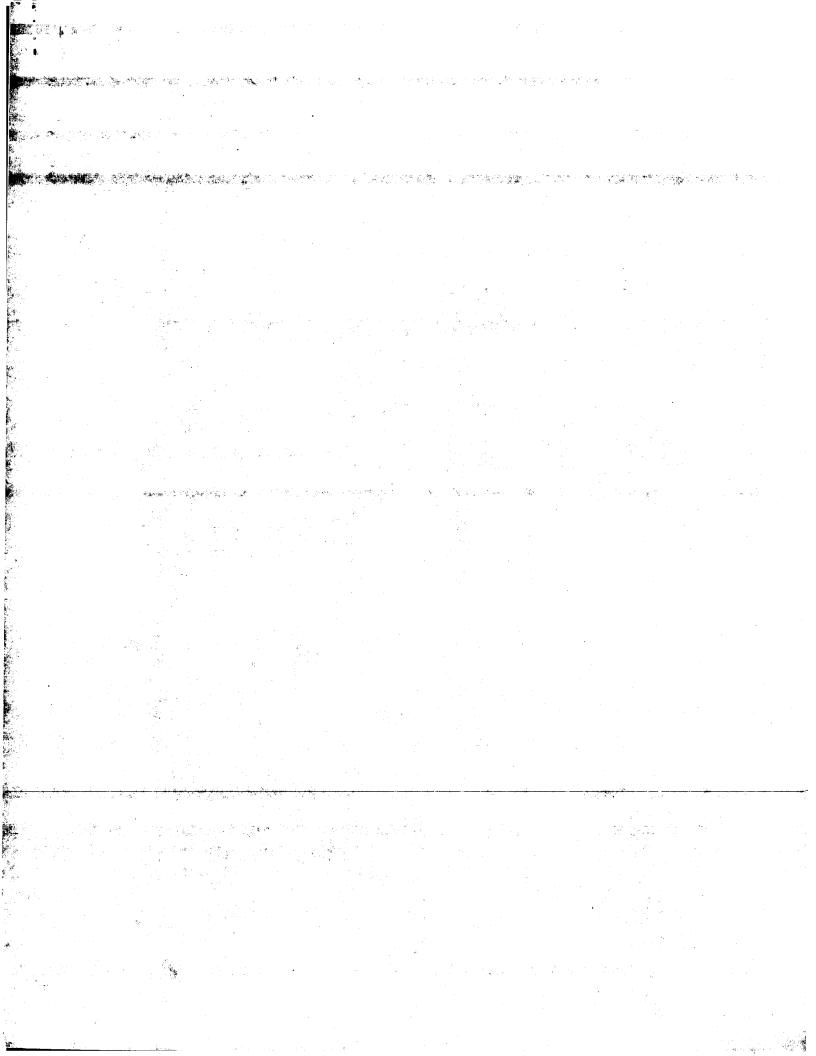
A;Accession: A71856
                                                                                                                                                                                                                                                                                  protein R09F10.5 [imported] - Caenorhabditis elegans
C;Speciles: Caenorhabditis elegans
C;Speciles: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
C;Accession: H89587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP synthase b' - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
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A71856
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A;Accession: A64662
                                                           A; Molecule type: DNA
A; Residues: 1-145 <S
                                                                                                   A; Status: preliminary
                                                                                                                        A;Title: Genome sequence of the nematode C. elegans: a platform A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_san A;Note: published errata appeared in Science 283, 35, 1999; Science A;Accession: H89587
                                                                                                                                                                                                                                       R;anonymous, The C. elegans (
Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                              C; Accession:
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A; Residues: 1-144 <Al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-144 <TOM>
                                        A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                       H89587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references:
                    Genetics
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R09F10.5
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                                                             <STO>
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                                      GB:chr_x;
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                                        PIDN: AAC69094.1;
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Pred. No.
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                                      PID:g1465853; GSPDB:GN00028;
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                                                                                                                                                 and www_sanger.ac.uk/Projects/C_
, 1999; Science 283, 2103, 1999;
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                                           CESP: R09F
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A;Cross-references: GB:AL591985; PIDN:CAC48757.1; PID:g15140230; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Peta, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A;Authors: Kahn, D.; Kahn, M. Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; pMID:11474104
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E95886
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                                                                                                                                                                                                                                                                     A; Contents: annotation
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A; Residues: 1-148 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: E95886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change
C:Accession: E95886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable sugar-phosphate isomerase protein [imported] - Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
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A;Molecule type: DNA
A;Residues: 1-145 <PAR>
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A;Accession: F81272
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1, S.; Barrel
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A;Status: preliminary
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hypothetical protein RC0191 [imported] - Rick C; Species: Rickettsia conorii C;Date: 30-Sep-2001 #sequence_revision 30-Sep C;Accession: G97723 R;Ogata, H.; Audic, S.; Renesto-Audiffren, P. Science 293, 2093-2098, 2001 A;Title: Mechanisms of Evolution in Rickettsi A;Reference number: A97700; MUID:21442074; PM A;Accession: G97723
                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: hsp
C;Superfamily: ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Skattor 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Bar A; Title: Deciphering the biology of Mycobacterium tuberculosis from A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Accession: G70939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: G70939
R; Cole, S.T.; Brosch, R.;
Connor, R.; Davies, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-159 < COL>
A; Cross references: GB: ALO21929; GB: AL123456;
A; Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable hsp protein - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
                                                                                                                                                                                            RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 2
A; Introns: 70/1; 100/3; 132/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CESP:F54D5.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source:
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A; Residues: 1-158 <WIL>
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                     ution in Rickettsia conorii and MUID:21442074; PMID:11557893
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                                                                                                                                                                                                                                                                                                                                             Score 121;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21; DB 2;
Pred. No. 3.3e+02;
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                                                                                                                                                  Rickettsia conorii (strain Malish
                                                                           P.; Fournier,
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                                     Rickettsia
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A;Molecule type: DNA
A;Residues: 1-159 <KUR>
A;Cross-references: GB:AE006914; PIDN:AAL02729.1; PID:g15619240; GSPDB:GN00173
A;Cross-references: GB:AE006914; PIDN:AAL02729.1; PID:g15619240; GSPDB:GN00173
A;Genetics:
B;Genetics:
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    protein search, using
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FTSQ.STRGR
HYB3_BRARE
ATKC_HALNI
OL11_HUMAN
U119_CAEELT
V1B8_AGRT19
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Query Match Best Local Matches

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the Swiss Institute pean Bioinformatics pean Bioinformatics and this statement requires a license an email to license an BAA35868 1; AL 10743; BAA358 1; AL 10743; BAA358 1; AL 10744 1; AL 10745 1; AL	FROM N.A. 12; 97061202; PubM 97061202; PubM 1, Aiba H., Ba 1, Ba 1, Ritagawa M. 1, Kitagawa M. 1, Kitagawa M. 1, Seki Y., Ta 1, Seki Y., Ta 1, Tabona sequence 1, DaNa sequence 1, DaNa sequence 1, Jan. 1, J	774; STAND/ (Rel. 36 (Rel. 36) (Rel. 40) (Rel. 40) (Coli. Coli. Coteobacte Coteobacte M N.A. MG1655; 2661655; 2661655; 27611ado-Vic Auris N.W O Y.; Coteobacte Coli. Col	00000000000
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ht. Bio Bio Situ Sib Sib TT.	55232; Fujita K., ., Kajiharano K., Masud ıra Y., Nashi ., Takemoto ., Takerichi	PRT;) quence up notation notation	Y625_TREPA RL7C_SCHPO SOJ_TREPA BIOC_TREPA BIOC_TREPA CAH2_CHICK EXL2_ARATH FLIP_CAUGC PANB_CORGL CYNT_SYNY3 YSI1_CAEEL SUHB_METTH DEGV_BACSU ALIGNMER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92134263; PubMed-1370883; Kamito T., Tanaka H., Sato B., Nagasawa H., Suzuki A.; Natuleotide sequence of cDNA for the eclosion hormone silkworm, Bombyx mori, and the expression in a brain." Biochem. Biophys. Res. Commun. 182:514-519(1992).
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01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Eclosion hormone precursor (Ecdysis activator)
Bombyx mori (Silk moth)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: NEUROPEPTIDE THAT TRIGGERS THE PERFORMANCE OF ECDYSIS BEHAVIORS AT THE END OF A MOLT. IT TRIGGERS ADULT BEHAVIOR PATTERNS: LARVAL, PUPAL AND ADULT ECDYSIS, AND PLASTICIZATION DURING THE MOLT.
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of the silkworm,
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MEDLINE=95115533; PubMed=7815924;
                                                                                                                                                                                                 Eukaryota;
                                                         Nielsen J.,
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Insecta; Pterygota;
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PRINTS; PR00159; 2FE2SFREDOXIN; PR0SITE; PS00197; 2FE2S_FERREDOXIN; 1.
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          Big flies,
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                                                                                                                                                                                                                    oxocera albisata (Rust fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M88251; AAA27329.1; -. PIR; C47673; C47673. HSSP; P27320; IDOX.
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-i- Cofactor: binds 1 2fe-2s cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the marine cyanobacterium Synechococcus sp. J. Gen. Microbiol. 138:1613-1621(1992).
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InterPro; IPR001041; Ferredoxin.
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"An iron stress operon involved in
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idea; Psilidae; Psilinae;
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01-NOV-1997
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1 NOISECT TRANSCRIPTIONAL INHIBITION (BY SIMILARITY).

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1 FIRST ACCUMULATES IN THE PERINUCLEAR REGION ABOUT ONE HOUR BEFORE TRANSLOCATION INTO THE NUCLEUS (BY SIMILARITY).

1 POMI: PHOSPHORULATED WITH A CIRCADIAN RHYTHMICITY, PROBABLY BY THE DOUBLE-TIME PROTEIN (DBT). PHOSPHORYLATED IN THE FORMATION OF HETERODIMER WITH THE FORMATION OF HETERODIMER PER TIME INTO THE MONOMER AND IN THE FORMATION OF HETERODIMER THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER THE STABILITY OF THE STABILITY OF THE STABILITY OF THE STABILITY OF THE STABILITY
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                                                             MEDLINE=97305158; pubMed=9161424; beakin W.J., Furniss C.S., parker V.E., Shaw "Isolation and characterisation of a linked Agrobacterium tumefaciens encoding proteins basal-body structure."; gene 189:135-137(1997).
                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=97305158; Pubme
Deakin W.J., Furniss C
                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat Flagellar basal-body rod protein flgC. FLGC OR ATU0554 OR AGR_C_975
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SEQUENCE FROM N.A. MEDLINE-21608550;
                                                                                                                                                                                                                                    Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                             Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biological rhythms; Repeat; Nuclear protein;
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109 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
  PubMed=11743193;
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| flagellar
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01-NOV-1995 01-NOV-1995 15-JUN-2002

(Rel. 32, Created)
(Rel. 32, Last sequence up
(Rel. 41, Last annotation
1 protein HI0589.

update)

update)

Hypothetical HI0589.

Haemophilus influenzae. Bacteria; Proteobacteria;

gamma

subdivision;

Pasteurellaceae;

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HAEIN

Y589_HA P44020;

HAEIN

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Cielo C. Slater S.;

Genome sequence of the plant pathogen and biotechnology agent agrows a sequence of the plant pathogen and biotechnology agent agrows a sequence 294:2323-2328(2011).

Science 294:2323-2328(2011).

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                                                                                                                                                    CONFLICT
SEQUENCE
                                                                                                                                                                                                                       EMBL; U39941; AAB68966.1; ...
EMBL; U95165; AAB71788.1; ...
EMBL; AE009024; AAA141571.1; ...
EMBL; AE007999; AAR86366.1; ...
Interpro; IPR001444; Flag_bb_rod.
PROSITE; PS00588; FLAGELLA_BB_ROD;
                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Filanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                   PROSITE; PS00588; FLAGELLA_B) Flagella; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=21608551;
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                                                                                                                                                                                         CONFLICT
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113 SYDA 116
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101
139 AA;
                                                                       100.0%; ilarity 100.0%; Conservative 0;
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15100
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                                                                                                                                                  IA -> MS (IN REF. 1).
L -> V (IN REF. 1).
; F94340FA0CF1D6B8 CR
                                                                         Score 21; DE
Pred. No. 1.1
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Matches 4
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                              Iida K.,
Yahara I.
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01-JUL-1993
01-JUL-1993
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TRANSMEM 71
TRANSMEM 97
SEQUENCE 139 AA;
                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF MEDITNE-93132073; PubMed-8421056; Moon A.L., Janmey P.A., Louie K.A., "Cofilin is an essential component cytoskeleton."; J. Cell Biol. 120:421-435(1993).
                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacclaromycetales; Saccharomycetaceae; Saccharomyces
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COF1 OR YLL050C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
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                                                                        SEQUENCE FROM N.A. MEDLINE=93178959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U32740; AAC22246.1; TIGR; HI0589; -.
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                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
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      Isolation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                           Cell Biol.
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(Rel. 26, Last sequence (Rel. 41, Last annotation)
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117
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Last annotation updat
  essential gene,
                                                Matsumoto S.,
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6C26821FAF4DF32D
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                                            Kawasaki H., Nishida
                                                                                                                                                                                                                                                      43-56;
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  COF1,
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ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                   yeast cortical
                                                                                                                                                                                                                                                      83-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.
that encodes a homologue
                                                                                                                                                                                                                                                                                                                                          Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                      AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B.A., Merrick J.M.,
Gocayne J.D.,
lev J M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inner
                                              H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT 8
SOD1_HALME

밁

49

SYDA 52

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SALARA SA
Qγ
                                                          Matches
                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z14971; CAA78694.1; -.
EMBL; D13230; BAA02514.1; -.
EMBL; Z73155; CAA97502.1; -.
PIR; A44397; A44397
PIR; S31309; S31309.
PIR; JN0529; JN0529.
PDB; 1COF; 01-APR-97
PDB; 1COF; 01-APR-97
PDB; 1CPY; 01-APR-99.
SGD; S0003973; COF1.
                                                                                                                                                                     Actin-binding; Cytoskeleton; 3D-structure.

DOMAIN 90 109 ACTIN-BINDING
SEQUENCE 143 AA; 15901 MW; 7A03747B0F2
                                                                                                                                                                                                                                                                                                        InterPro; IPR002108; Actbind_cofln.
Pfam; PF00241; cofilin_ADF; 1.
ProDom; PD002129; Actbind_cofln; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                   SMART; SM00102; ADF; 1.
PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib!ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fedorov A.A., Lappalainen P., Fedoróv E.V., "Structure determination of yeast cofilin."; Nat. Struct. Biol. 4:366-369(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             x-ray Crystallography (2.3 angstroms).
medLine=97290449; pubmed=9145106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rodal A.A., Tetreault J.W., Lappalainen P., I "Aiplp interacts with cofilin to disassemble J. Cell Biol. 145:1251-1264(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.";
Gene 124:115-120(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of mammalian cofilin, a low-M(r) actin-binding and depolymerizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10366597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Interacts with actin and AIP1 in a ternary complex. SUBCELLULAR LOCATION: THROUGHOUT THE CYTOPLASM (BUT NOT ON T CYTOPLASMIC CABLES) AND MAJOR COMPONENT OF THE CORTICAL ACTICYTOSKELETON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: THE N-TERMINUS SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION AND EDPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO BEPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO BIND G- ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN IT IS THE MAJOR COMPONENT OF INTRANUCLEAR AND CYTOPLASMIC ACTIN RODS. IN EFFECT, YEAST COFILIN INCREASES THE RATE OF ACTIN POLYMERIZATION BY MAKING NEW ENDS AVAILABLE FOR ACTIN SUBUNIT ADDITION. SUCH A PROTEIN COMPLEX IS IMPORTANT FOR THE POLARIZED GROWTH OF YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: THE N-TERMINUS IS BLOCKED, SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEIN SIMILAR TO THE N-TERMINUS OF YEAST ABPI PROTEIN.
SYDA 4
                                                          4;
                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wedler E., (MAY-1996)
                                                          Conservative
                                                                                                                                                               109 A
; 15901 MW;
                                                                                 100.0%;
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To the EMBL/GenBank/DDBJ
                                                          0;
                                                                                                                                                                  ACTIN-BINDING (POTENTIAL); 7A03747B0F21F22D CRC64;
                                                                                 Score 21;
Pred. No.
                                                 Mismatches
                                                    1.2e+02;
thes 0;
                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drubin D.G., Amberg D.C. e actin filaments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drubin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEINS
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                                                                                                        Length 143;
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                                                       0;
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                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE
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STANDARD;

PRT;

144

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GALX_CANA
A
ID GALX_C
A
AC P56600
DT 15-DEC
DT 15-DEC
DT 15-DE
C GAL10
DE GAL10
DE (EC 5.
DE (Mutar
GN GAL10
OS Candid
OC Eukary
OC Saccid
ON NCBI_T
RN [1]
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                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                         GALX_CANMA STAN
P56600;
15-DEC-1998 (Rel. 3
15-DEC-1998 (Rel. 3
15-JUN-2002 (Rel. 4
     Eukaryota; Fung1; Ascomycota;
Saccharomycetales; mitosporic
NCBI_TaxID=5479;
                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAL10 bifunctional protein [Includes: UDP-glucose 4-
(EC 5.1.3.2) (Galactowaldenase); Aldose 1-epimerase
(Mutarotase)] (Fragment).
                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: U78908; AAB60932.1; -.
HSSP; P80857; ISSS.
InterPro; IPR0011189; SODIsmutase.
Pfam; PF00081; sodfe; 1.
Pfam; PF02777; sodfe_C; 1.
                                                                                                                                                                                                                                                                                                                                             METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ell the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Superoxide dismutase [Mn] 1 (EC 1.15.1.1) (Fragment).
SOD1.
                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          archaea.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97257269; PubMed=9106366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Halo Halobacteriaceae; Haloferax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOD1_HALME
008461;
                                                                                                                                                                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Evolutionary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dennis P.P., Shimmin L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Halobacterium mediterranei (Haloferax
                                                                                                                                                                                                                        71 SYDA 74
                                                                                                                                                                                                                                                \vdash
                                                                                                                                                                                                                                    L SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                        PD000475; SODismutase; PS00088; SOD_MN; 1.
                                                                                                                                                                                                                                                                      4.
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                   1
42
124
128
144
144
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      divergence and salinity-mediated
                                                                                                                                                                                                                                                                                                                      Ą,
                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                              Manganese.
                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                      15613 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Halobacteria;
                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                             MANGANESE LIGAND
MANGANESE LIGAND
                                                                                                                                                                                                                                                                                  Score 21;
Pred. No.
                         Saccharomycotina;
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                      47BBA0AC551A09A4 CRC64;
                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                            153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mediterranei)
                                                                                                                                                                                                                                                                      1.2e+02;
thes 0;
                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      selection
                         Saccharomycetes; Candida.
                                                                                                                                                                                                                                                                                            Length 144;
                                                                                    4-epimerase
se (EC 5.1.3.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ί'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      halophilic
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                                                                                                                                                                                                                                                                      Gaps
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RESULT 10
                                                                                                                                                                                                                                                                                                                        Вb
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                                                                                                                                                                                                                                                                      RIB2_PHOLE
                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIB2_PHOLE Q93E92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01370; Epimerase; 1.
Pfam; PF01370; Epimerase; 1.
PROSITE; PS00545; ALDOSE_1_EPIMERASE; PARTIAL.
PROSITE; PS00545; ALDOSE_1_EPIMERASE; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D29759; -; NOT_ANNOTATED_CDS.
HSSP; P09147; IXEL.
InterPro; IPR001823; Ald1_epimerase.
InterPro; IPR001823; Epimerase_Dh.
InterPro; IPR00205; NAD_binding.
InterPro; IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Park S.M., Ohkuma M., Masuda Y., Ohta A., Takagi M.;
"Galactose-inducible expression systems in Candida maltosa
promoters of newly isolated GAL1 and GAL10 genes.";
Yeast 13:21-29(1997).
                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2
(Lumazine synthase) (Riboflavin synthase beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                +
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97197967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                        40 SYDA 43
                                                                                                                                                                                                                                                                                                                                                1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: Galactose metabolism; third step.
PATHWAY: Hexose metabolism.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPIMERASE FAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE ALDOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Mutarotase converts alpha-aldose to the beta-anomer. is active on D-glucose, L-arabinose, D-xylose, D-galactose,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPIMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                        h 100.0%;
Similarity 100.0%;
4; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                           153
153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galactose metabolism; third step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         enzyme;
>153
                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9046083;
                                                                                                                                                                                                                                                                                                                                                                                                                           16752
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isomerase; NAD; Galac
GALACTOWALDENASE
                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                      Score 21;
Pred. No.
                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                           A069AC3040BC978D
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                        156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UDP-galactose
                                                                                                                                                                                                                                                                                                                                                                                    1.2e+02;
                                                                                                                                                                                                                                                        æ
                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta-D-glucose
                                                                                                                                                                                                                                                                                                                                                                                                Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metabolism
                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE SUGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   using
                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                        0;
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Lin J.-W., Chao Y.-F., Weng S.-F., TibB, ribH, ribA reside "Riboflavin synthesis genes ribE, ribB, ribH, ribA reside operon of photobacterium leiognathi.";
Biochem. Biophys. Res. Commun. 284:587-595(2001).

'n

the

Riboflavin synthase is a bifunctional enzyme

STRAIN=PL741; MEDLINE=21290647; PubMed=11396941;

Photobacterium. NCBI_TaxID=658;

SEQUENCE

FROM N.A.

Photobacterium leiognathi

Bacteria; Proteobacteria;

gamma

subdivision; Vibrionaceae;

2.5.1.9) 1 chain).

(DMRL

synthase)

RIBH.

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RESULT 11

RESULT 11

RAC P4116

DT 01-FI

DT 01-FI

DT 01-FI

DT 01-FI

DT 01-FI

DT 01-FI

CO Tryp

CO STRYP

CO -1

CC -1

CC Th

CC -1

CC -1
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Best Local :
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P41165;
01-FEB-1995 (Rel. 31, L
01-FEB-1996 (Rel. 33, L
01-FEB-1996 (Rel. 33, L
                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                MEDLINE-94232821; pubMed-8177742;
Metzenberg S., Joblet C., Verspieren P., Agabian
"Ribosomal protein L25 from Trypanosoma brucei: p
molecular co-evolution of an rRNA-binding protein
binding site.";
Nucleic Acids Res. 21:4936-4940(1993).
-1- FUNCTION: THIS PROTEIN BINDS TO A SPECIFIC RE
                   EMBL; L21172; AAC37186.1; -.
InterPro; IPR001014; Ribosomal_L23.
Pfam; PF00276; Ribosomal_L23; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-ISTAT
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRYBB_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trypanosoma brucei brucei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPL23A OR RPL25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riboflavin biosynthesis; Transferase SEQUENCE 156 AA; 16423 MW; B53E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002180; DMRL_synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGRO0114; ribh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF364106; AAK83294.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SYDA 4
                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By similarity). CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
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             Ribosomal_L23;
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PROTEIN BINDS TO A
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Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 AA
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HXD3_BRARE
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                                                                                    DNA_BIND
NON_TER
SEQUENCE
                                                                                                                                                                                              PRINTS; PRO0024; HOMEOBOX.
PRINTS; PRO0031; HTHREPRESSR.
PRINTS; PRO0031; HTHREPRESSR.
PRO00010: Homeobox; 1.
                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                         Transcription NON_TER
                                                                                                                                                             PROSITE; PS00027; HOMEOBOX_1; PROSITE; PS50071; HOMEOBOX_2;
                                                                                                                                                                                      ProDom; PD000010; Homeobox; SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                 ZFIN; ZDB-GENE-990415-120; hoxd3a.
InterPro; IPR000047; HTH_repressr.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prince V.E., Moens C.B., Kimmel C.B!, Ho R.K.;

"Zebrafish hox genes: expression in the hindbrain region of wild-type and mutants of the segmentation gene, valentino.";

Submitted (JUN-1997) to the EMBL/GehBank/DDBJ databases.

-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY
                                                                                                                                        PROSITE; PS50071; HOMEOBOX_2; 1.
Homeobox; DNA-binding; Developmental
                                                                                                                                                                                                                                                                                         EMBL; Y13948; CAA74286.1; -. TRANSFAC; T03651; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyprinidae;
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O42370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38,
15-JUL-1999 (Rel. 38,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00050; RIBOSOMAL_L23; 1.
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1 SYDA 4
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                                   Similarity 4; Conser
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167
167
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164 AA;
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                                                                                                                                    regulation.
                                                                                   AA;
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                                                                                   18339
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18170 MW; 1606F4E8BFCE0C8F CRC64;
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Pred. No.
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                                                                                  E9032/3377FF865CF CRC64;
                                  Mismatches
                                                                                                                                            protein; Nuclear protein;
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                                              1.4e+02;
                                                         DB 1;
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                                                         Length 167;
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71

SYDA

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S2_MESC.

RBS2_MESCR

2 Q04450;

7 01-OCT-1994 (Rel. 30, Created)

T 01-OCT-1994 (Rel. 30, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

T 16-OCT-2001 (Rel. 40, Last annotation update)

Tibulose bisphosphate carboxylase small chain 2,

Tibulose bisphosphate carboxylase small chain 2,
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                                                                                                                                                                                                                                                     RESULT 14
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Best Local S
Matches 4
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O14434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOI. Microbiol. 26:175-183(1997).

- FUNCTION: MODULATES THE BLUISH-GREEN PIGMENTATION OF CONIDIA

- BULL AS COMPLEMENT DEPOSITION.

- CATALYTIC ACTIVITY: Scytalone = 1,3,8-trihydroxynaphthalene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASPFU
                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004235; Scytalone_DH
Pfam; PF02982; Scytalone_DH; 1.
Lyase; Conidiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U95042; AAC49843.1; -. HSSP; P56221; 3STD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Aspergillus fumigatus arpl modulates complement deposition.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98043547; PubMed=9383199;
Tsai H.-F., Washburn R.G., Chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000
30-MAY-2000
             SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus fumigatus (Sartorya fumigata).
 MEDLINE-93302719;
                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                             1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY: BIOSYNTHESIS OF FUNGAL BLUISH-GREEN PIGMENT. DEVELOPMENTAL STAGE: EXPRESSED DURING CONIDIATION.
                                                                                                                                                                                                                                                                                                SYDA 31
                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  168 AA;
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(Rel. 39, Last sequence update)
(Rel. 39, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                        Caryophyllales;
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 PubMed=8316216;
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dehydratase (EC 4.2.1.94).
                                                                                                                                                                                                                                                                                                                                                                                                                  19716 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chang Y.C.,
                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                    Score 21; DB 1;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  F40C22CEB6D02695 CRC64;
                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Kwon-Chung
conidial pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions ong as its content is in
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                                                                                                   plant)
                                                                                                                                              2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pigmentation
                                                                                                                                                                                                                                                                                                                                                                                   Length 168;
                                                                                                                                             chloroplast precursor
                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONIDIA AS
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Best Local S
Matches 4
Luxaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Aizoaceae: Mesembruna: NCBI_TaxID=3544;
                                                                              01-APR-1990 (Rel. 14, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ribulose bisphosphate carboxylase small chain
(EC 4.1.1.39) (RuBisCO small subunit 1).
RBCS-1 OR RBCS OR RBCS.
                                                                                                                                                                                RBS1_MES
                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Derocher E.J., Quigley F., Mache R., Bohnert H.J.;
"The six genes of the Rubisco small subunit multigene family
Mesembryanthemum crystallinum, a facultative CAM plant.";
Mol. Gen. Genet. 239:450-462(1993).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L10214; AAA03694.1; -.
EMBL; M38316; AAA33036.1; -.
EMBL; S35246; S35246.
Fir; S35246; S35246.
InterPro; IPR000894; RuBisCO_small.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commentations of the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Physiol. 95:976-978(1991).

-I: FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00101; RuBisCO_small; 1.
PRINTS; PR00152; RUBISCOSMALL.
ProDom; PD000290; RuBisCO_small;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carboxylase/oxygenase small subunit gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Derocher E.J., Michalowski C.B., Bohnert H.J.; "cDNA sequences for transcripts of the ribulose-1,5-bisphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lyase; Oxidoreductase; Monooxygenase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Photosynthesis;
                                                                                                                                                                                                                                                                            177 SYDA 180
                                                                                                                                                                                                                                                                                                               1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-phospho-D-glycerate + 2-phosphoglycolate.
SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
SUBCELLULAR LOCATION: Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phospho-D-glycerate.
CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) - 2
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                                                                                                                                                                                                                                                                                                                                             4.
                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           154
180 /
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          56
                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carbon dioxide fixation; Photorespiration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RuBisCO_small; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           154
20084 MW;
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180
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RIBULOSE BISPHOSPHATE CARBO
                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN 2.
                                                                                                                                                                                                                                                                                                                                                           Score 21; DB 1;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                          -> I (IN REF. 2).
6977DC72C89940F3 CRC64;
                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                 182
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                                                                                                                 chloroplast precursor
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                                                   Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide;
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ATPD_BACHD
ID ATPD_B
AC Q9K6H2
DT 16-OCT
DT 16-JUN
DT 15-JUN
DT ATP SYN
GN ATPH O)
OS Bacill
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Best Local
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                        ATPD_BACHD Q9K6H2;
Q9K6H2;
16-OCT-2001 (Re
16-OCT-2001 (Re
15-JUN-2002 (Re
ATP synthase de
ATPH OR BH3757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
SEQUENCE
    Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A29118; RKIXS.

PIR; S35247; S35247.

InterPro; IPR000894; RuBisCO_small.

Pfam; PF00101; RuBisCO_small; 1.

PRINTS; PR00152; RUBISCOSMALL.

ProDom; PD000290; RuBisCO_small; 1.
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                                                                                                                                                                                                                                                                               179 SYDA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Photosynthesis; Carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L10212; AAA03693.1; -. EMBL; M31640; AAA33035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mesembryanthemum crystallinum.";

Nucleic Acids Res. 15:6301-6301(1987).

-I- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSEHATE, THE PRIMARY EVENT IN PHOTOSYNVHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE PRAGMENYATION (THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyase; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Derocher E.J., Quigley F., Mache R., Bohnert H.J.;
"The six genes of the Rubisco small subunit multigene family Mesembryanthemum crystallinum, a facultative CAM plant.";
Mol. Gen. Genet. 239:450-462(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Derocher E.J., Ramage R.T., Michalowski "Nucleotide sequence of a cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=87316892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93302719; PubMed=8316216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE
                                                                                                                                                                                                                                                                                                                             1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its produced institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phospho-D-glycerate.

CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2)
3-phospho-D-glycerate + 2-phosphoglycolate.
SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
SUBCELLULAR LOCATION: Chloroplast.
SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIVE SITE.

CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) =
                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family.
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145
182 /
                                                                 (Rel. 40, Created)
(Rel. 40, Last sequence (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                              delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΑA;
                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RUBLISCO_Small; 1.
arbon dioxide fixation; Photorespiration; arbon dioxide fixation; Chloroplast; Transit
                                                chain
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145
E
20276 MW;
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182
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                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                 Last sequence update)
Last annotation updat
lain (EC 3.6.3.14).
                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                   Score 21; DB 1;
Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                        183
                                                            update)
                                                                                                                                                        A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bohnert
from the
                                                                                                                                                                                                                                                                                                                                                                                                        Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOXYLASE SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H.J.;
desert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide;
                                                                                                                                                                                                                                                                                                                                                          0,
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                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT
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Best L
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=93302719; PubMed=8316216; |

MEDLINE=93302719; PubMed=8316216; |

Derocher E.J., Quigley F., Mache R., Bohnert H.J.;

"The six genes of the Rubisco small subunit multigene family

"The six genes of the Rubisco small subunit multigene family

"The six genes of the Rubisco small subunit multigene family

"The six genes of the Rubisco small subunit multigene family

"The six genes of the Rubisco small subunit multigene family
                                                                                                                                                                                                    RBS3_MESCR STANDARD; PRT; 183 AA. 008183; 01-0CT-1994 (Rel. 30, Created) 01-0CT-1994 (Rel. 30, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Ribulose bisphosphate carboxylase small chain (EC 4.1.1.39) (RuBisco small subunit 3).
                                                                                                                                                                                                                                                                                                                              MESCR
                                                                                                                             Mesembryanthemum crystallinum (Common ice plant).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Caryophyllidae; Caryophyllales; Alzoaceae; Mesembryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0125; ATPASEDELTA.
TIGRFAMS; TIGR01145; ATP_synt_deltd; 1.
PROSITE; PS00389; ATPASE_DELTA; 1.
Hydrolase; ATP synthesis; CF(1); Hydrogrouplete proteome.
SEQUENCE 183 AA; 20605 MW; 5CR79900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not|removed entities requires a license agreement (See lor send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000711; ATPsynt_OSCP. Pfam; PF00213; OSCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP001519; BAB07476.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., SaFuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                      101 SYDA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicu
NCBI_TaxID=86665;
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                                                                                                                                                                                                                                                                                                                                                                                                                    1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1).
HAS THREE MAIN SUBUNITS: A, B AND C.
SIMILARITY: BELONGS TO THE ATPASE DELTA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H(+)(Out).

SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE COMPONENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillales; |Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21; DB 1;
Pred., No. 1.5e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5CB7989AFA5D26F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                             Mesembryanthemum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ion transport;
                                                                                                                                                                                                                           ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asaki R.,
Kuhara S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 183;
                                                                                                                                                                                                                      chloroplast precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP + phosphate
                                                                                                                                              eudicots;
                                                                                                                                                           Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHANGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Masui N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
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                                                                                                                                                                                                                                                                                    RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                 Ol-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ribulose bisphosphate carboxylase small chain
(EC 4.1.1.39) (RuBisCO small share)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Derocher E.J., Michalowski C.B., Bohnert H.J.;
"CDNA sequences for transcripts of the ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit gene family of Mesembryanthemum crystallinum.";
Plant physiol. 95:976-978(1991).
-!- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000894; RuBisCO_small.
Pfam; PF00101; RuBisCO_small; 1.
PRINTS; PR00152; RUBISCOSMALL.
ProDom; PD000290; RuBisCO_small; 1.
                                                                                                                                                                                                                  RBS6_MESCR STA
Q08186;
Q1-OCT-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L10215; AAA03695.1;
EMBL; M38317; AAA33037.1;
PIR; S35245; S35245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
              SEQUENCE FROM N.A. MEDLINE-93302719; PubMed-8316216;
                                                                          Mesembryanthemum crystallinum (Common ice plant).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magonolophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Photosynthesis; Carbon dioxide fixation;
                                                                                                                                            RBCS-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lyase; Oxidoreductase; Monooxygenase;
                                                                                                                                                                                                                                                                                                                                  180 SYDA 183
                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 4; Conserv
                                                                                                                                                                                                                                                                                                                                                              1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) phospho-D-glycerate.
CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) 3-phospho-D-glycerate + 2-phosphoglycolate.
SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
SUBCELLULAR LOCATION: Chloroplast.
SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
E.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 t
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59
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                                                                                                                                                                                                                                                    STANDARD;
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183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85
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 F., Mache R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN 3.
M -> I (IN REF.
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RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL
                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         F056AAA5B110AA71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               21;
No.
                                                                                                                                                                                                                                                      186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                             1.5e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Photorespiration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2)
                                                                                                                                                                      6, chloroplast precursor
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 183;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide;
                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 3-
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                        obtained by genetic Proc. Natl. Acad. So-1- FUNCTION: Destro
                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=CV. P2;
                                                                                                                                                                                                                                                                                                                    SODB.

Nicotiana plumbaginifolia (Leadwort-leaved tobacco).

Nicotiana plumbaginifolia (Leadwort-leaved tobacco).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L10213; AAA03698.1; -.
PIR; S35242; S35242.
InterPro; IPR000994; RuBisCO_small.
Pfam; PF00101; RuBisCO_small; 1.
PRINTS; PR00152; RUBISCO_small; 1.
ProDom; PD000290; RuBisCO_small; 1.
ProDom; PD000290; RuBisCO_small; 1.
Photosynthesis; Carbon dioxide fixation; Photorespiration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryop
Spermatophyta; Magnoliophyta; eudicotyledons; c
Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1991 (Rel. 19,
01-AUG-1991 (Rel. 19,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SODF_NICPL P22302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyase; Oxidoreductase; Monooxygenase; Multigene family.
TRANSIT 1 61 CHLOROPL
                                                                                                                                                                                                         STRAIN-CV.
                                                                                                                                                                                                                                                                                 NCBI_TaxID=4092;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Superoxide dismutase [Fe],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷
                                                                                                                                                      van Camp W.,
                                                                                                                                                                           MEDLINE=91088619; PubMed=2263641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÷
                                                                                                "Characterization of iron superoxide dismutase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 SYDA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-phospho-D-glycerate + 2-phosphoglycola
SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS
SUBCELLULAR LOCATION: Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phospho-D-glycerate.
CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
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                                                                                                                                                   Bowler C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                  enetic complementation in Escherichia coli.", cad. Sci. U.S.A. 87:9903-9907(1990).
Destroys radicals which are normally produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
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186
are toxic to
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Last sequence update)
Last annotation update)
[Fe], chloroplast (EC 1.15.1.1) (Fragment).
                                                                                                                                                      Villarroel R., Tsang E.W.T.,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5e+02;
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                                                                                                                                                      Montagu
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                          within
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RESULT 20 FLID_PROMI
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Best Local S
Matches 4
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or send a
                                                                                                                     "Sequence and genetic analysis of multiple flagellin-encoding from Proteus mirabilis.";
Gene 148:33-41(1994).
                                                                                                                                                                                                                                                                                              FLID_PROMI STANDARD; PRT; 205 AA. P42274; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Flagellar hook-associated protein 2 (HAP2) (Final Protein 2 (HAP2))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; P0000475; SODismutase; 1.
PROSITE; PS00088; SOD_MN; 1.
Oxidoreductase; Iron; Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-!- COFACTOR: Iron.
-!- SUBGUNIT: HOMODIMER.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- INDUCTION: BY ENVIRONMENTAL CONDITIONS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A39267
HSSP; P0915
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                                                                                                                                                              Belas R., Flaherty
                                                                                                                                                                                      STRAIN-BB2000;
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      Proteus
                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                             FLID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M55909; AAA34074.1; -.
                                                                                                                                                                         MEDLINE-95011656; PubMed-7926835;
                                                                                                                                                                                                                         NCBI_TaxID=584;
                                                                                                                                                                                                                                                               Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
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                                                                                                                                                                                                                                                                                     (Flagellar cap protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                             107 SYDA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SYDA 4
                    FUNCTION: REQUIRED FOR THE MORPHOGENESIS AND FOR THE ELONG THE FLAGELLAR FILAMENT BY FACILITATING POLYMERIZATION OF FLAGELLIN MONOMERS AT THE TIP OF GROWING FILAMENT. FORMS A STRUCTURE, WHICH PREVENTS FLAGELLIN SUBUNITS (TRANSPORTED THE CENTRAL CHANNEL OF THE FLAGELLUM) FROM LEAKING OUT WIT POLYMERIZATION AT THE DISTAL END (BY SIMILARITY). SUBUNIT: HOMOPENTAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A39267; A39267.
P09157; 1ISC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00081; sodfe; 1.
PF02777; sodfe_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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78
162
166
202
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           BELONGS TO THE FLID FAMILY.
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D; Mismatches
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SIMILARITY).
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RESULT 21
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ID FTSQ_STRGR
AC P45503;
DT 01-NOV-1995
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Matches 4; Conser
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30-MAY-2000
Cell divisio
                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                             MEDLINE=94374704; PubMed=8088545; bharmatilake A.J., Kendrick K.E.; "Expression of the division-controlling gene ftsZ during growth sporulation of the filamentous bacterium Streptomyces griseus."; Gene 147:21-28(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces
Bacteria; Act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flagella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF221596; AAA62395.1;
                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).-i- SIMILARITY: BELONGS TO THE FTSQ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales;
NCBI_TaxID=1911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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153 SYDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SYDA 4
                      1 SYDA 4
                                                                                                                                                                                                                                                                                                                  FUNCTION: THIS PROTEIN MAY BE INVOLVED
                                                                                                                                                                                                                                                                                                        SIMILARITY).
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                                                                                                                                     division;
                                                                                                                                                   U07344; AAA56888.1;
                                                                                                                                                                         non-profit institutions as long and this statement is not removed. s requires a license agreement (See lan email to license@isb-sib.ch).
                                                           Similarity
156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ces griseus.
Actinobacteria; Actinobacteria (class); Actinobacteridae;
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205 AA;
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on protein
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ilarity 100.0%;
Conservative 0
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21942
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22281 MW;
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Last annotation update)
ftsQ homolog (Fragment).
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7CC9A86699746E82
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Pred. No.
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                                                                                                 (POTENTIAL)
6E82 CRC64;
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                                                                        Length 208;
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RESULT 22
HXB3_BRARE
                                                            Matches
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Best Local
                                                                                                                           DNA_BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prince V.E., Moens C.B., Kimmel C.B., Ho R.K.; "Zebrafish hox genes: expression in the hindbrain region of wild-type and mutants of the segmentation gene, valentino."; Development 125:393-406(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Actinopterygii; Neopterygii; Teleostei; Osta
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HXB3_BRARE STANDARD; PRT; 210 AA 042368; 15-JUL-1999 (Rel. 38, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat Homeobox protein Hox-B3 (Fragment).
                                                                                                                                                                                                   PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                   ProDom; PD000010; Homeobox; 1. SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                               PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
                                                                                                                                                                                                                                                                                                  Pfam; PF00046; homeobox;
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                                                                                                                                                      Transcription regulation.
                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                                               InterPro; IPR000047; HTH_repressr.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                ZFIN; ZDB-GENE-990415-104; hoxb3a.
                                                                                                                                                                                                                                                                                                                                                                TRANSFAC; T03631;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98165394; PubMed-9425135;
                                                                                                                                                                                         Homeobox;
 69
                                                            Local Similarity es 4; Conserv
                             1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN RHOMBOMERES 6 IN THE DEVELOPING HINDBRAIN DURING EMBRYOGENESIS. SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
FUNCTION: SEQUENCE-SPECIFIC TRANSPORT DESCRIPTION EACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
SUBCELLULAR LOCATION: Nuclear.
SYDA 72
                                                                                                                                                                                    DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                         210 /
                                                            Conservative
                                                                                                                           8
                                                                                                                         32 F
22862 MW;
                                                                        100.0%;
                                                           Score 21; DE
Pred. No. 1.7
0; Mismatches
                                                                                                                         HOMEOBOX.
; 55B0D2D2D79B8601 CRC64;
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hes 0;
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Ostariophysi; Cypriniformes;
                                                                                           DB 1;
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RESULT 23

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NG W.V., Kennedy S.P., Mahairas G.G., Berguist B., Pan M.,
NG W.V., Kennedy S.P., Mahairas G.G., Berguist B., Pan M.,
NG W.V., Kennedy S.P., Mahairas G.G., Berguist B., Pan M.,
NG W.V., Kennedy S.P., Mahairas G.G., Berguist B., Roog Y.A.,
NG Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
NG Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
NG Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
NG Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
NG Leithauser B., Keiler K., Cruz R., Dahl M.J., Hough D.W.,
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NG Leithauser B., Keiler K., Cruz R., Dahl D.,
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NG Leithauser B., Keiler M., Hold N., J., Hold D.,
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P67687;
P67687
                  OLII_HUMAN STANDARD; PRT; 216 AA. P47889; 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 01-factory receptor-like protein OR17-207 (Fragment). Homo sapiens (Human).
                                                                                                                                                                                                                                                                                            _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02669; KdpC; 1.
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Plasmid pNRC200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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23768 MW;
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Pred. No. 1.8e+02;
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Best Local
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SEQUENCE FROM N.A.
MEDLINE-97149282; PubMed-8996090;
Maduro M.F., Pilgrim D.B.;
"Conservation of function and expression of unc-119 from two
"Caenorhabditis species despite divergence of non-coding DNA.";
                                                                                                                                                              Q17297;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
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TRANSMEM
                                                                                 Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                     Caenorhabditis briggsae.
                                                                                                                    UNC-119
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Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Olfactory receptor gene cluster on human duplication of an ancestral receptor reper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94272458; PubMed-8004088;
Ben-Arie N., Lancet D., Taylor C.,
Ledbetter D.H., Carrozzo R., Patel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-94272458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lication of an ancestral receptor rep. Mol. Genet. 3:229-235(1994).
FUNCTION: PUTATIVE ODORANT RECEPTOR.
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                          SYDA
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. 35, Last sequence. 40, Last annotation.
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G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane;
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                                                                                            Nematoda; Chromadorea;
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                                                                                 Caenorhabditis
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CYTOPLASMIC (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (
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5 (POTENTIAL).
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K., S
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Sheer D., Lehrach
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UNC-119 OR M142.1.
Caenorhabditis elegans
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01-OCT-1996 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as slong as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib,ch).
          WormPep; M142.1; CE06203.
Developmental protein.
                                EMBL; U32854; AAC46919.1; -. EMBL; 273428; CAA97807.1; -.
                                                                   entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                       use
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                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                        STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          Maduro M.F., Pilgrim D.B.;
"Identification and cloning of unc-119,
Caenorhabditis elegans nervous system.";
Genetics 141:977-988(1995).
                                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
MEDLINE=96129273; PubMed=8582641;
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a ( between the Swiss Institute of Bioinformatics and the EMBL
                                                                                           modified
                                                                                                                              between
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                                                                                                                                                                                                                                             McMurray A.;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
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                                                                                                                European Bioinformatics Institute.
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                                                                                                                                                                                                             NERVOUS SYSTEM.
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                                                                                                                           the Swiss Institute of Bioinformatics
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34, Last sequence up
40, Last annotation
                                                                                                                                                                                    CITY: PREDOMINANTLY NEURON-SPECIFIC MUTATIONS IN UNC-119 CAUSE DIVERSE
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OR FUNCTION
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26F43457C5CDEB45 CRC64;

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YPVA_METTF
ID YPVA_METTF
YPVA_METTF
ID YPVA_METTF
YPVA_METTF
AC P29577;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Hypothetical 24.7 kDa protein (ORF5A).
OS Methanobacterium thermoformicicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
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Best Local Similarity
Matches 4; Conserv
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Y945_METJA
Q58355;
01-NOV-1997
01-NOV-1997
16-CCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus Jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entitles requires a license agreement (See http://www.isb-slb.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U67538; AAB98955.1; TIGR; MJ0945; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                jannaschii.";
Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical MJ0945.
                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Transmembrane; Complete proteome TRANSMEM 21 41 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanococcus jannaschii.
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                          Score 21; DB 1;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                1E9FF7E32C025DA9 CRC64;
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RESULT
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Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01345; DUF11; 1.
Hypothetical protein; Plasmid.
SEQUENCE 227 AA; 24681 MW;
                                  the European Bioinformatics Institute. There are no rest use by non-profit institutions as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                   This
                                                                                                                                             Plasmid pTi15955.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                   VIRB8
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P05357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93126090; PubMed=1336177;
Moelling J., van Eeden F.J.M., Eggen R.I.L., de Vos W.M.;
Modular organization of related Archaeal plasmids encoding
restriction-modification systems in Methanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-DSM 3848 / THF;
                                                                                                                                                                                                                                                                                                               Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                        Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                VirB8 protein
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PIR; S26440; S26440.
PIR; S30305; S30305.
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                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20:6501-6507(1992).
                                                                                                                                                                                                                                                                                                                           alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                       (strain 15955).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Pred. No. 1.9
); Mismatches
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s 0;
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                                                                                                                                                           ACT AT THE BACTERIAL IN DIRECTING T-DNA
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EMBL; X06826; CAC15165.1;

ALT_INIT

(See http://www.isb-sib

.ch/announce/

S00784; B8AG55

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RESULT 31
Y416_CHLTR
ID Y416_C
AC 084421
DT 16-OCT
DT 16-OCT
DT 16-OCT
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VIB8_AGRTU
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Best Local :
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Best Local
   Y416_CHLTR
084421;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                               Crown gall
                                                                                                                                                                                                                    EMBL; J03216; -; NOT_ANNOTATED_CDS. PIR; I28621; B8AGA6.
                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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P09781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989 (Rel. 10, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                       104 SYDA 107
                                                                                                                                                                                                                                                                                                                                                                                         Ward J.E.,
Nester E.W.
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90170994; PubMed=2307685;
Ward J.E., Akiyoshi D.E., Regier
                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                              tumefaciens Ti plasmid.";
J. Biol. Chem. 263:5804-5814(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of the virB operon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ward J.E., Akiyoshi D.
Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88186901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; alpha
Rhizobiaceae; Rhizobium.
NCBI_TaxID=358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobacterium Plasmid pTiA6
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SEQUENCE
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                                                                                                                              1 SYDA 4
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                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 265:4768-4768(1990).
FUNCTION: VIRB PROTEINS ARE SUGGESTED TO SURFACE AND THERE PLAY AN IMPORTANT ROLE TRANSFER TO PLANT CELLS.
                                                                                                                                                   4,
                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                   an email to license@isb-sib.ch)
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  (Rel. 40, Created)
(Rel. 40, Last sequence)
(Rel. 40, Last annotation)
                                                                                                                                                                                             tumor; Plasmid.
230 AA; 25382 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor; Plasmid
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                                               STANDARD;
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hi D.E., Regier
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Last sequence update)
Last annotation updat
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Pred. No.
                                              PRT;
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Pred. No.
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                                             236
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhizobiaceae group;
                                                                                                                                                                    Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                  Gordon
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RESULT 32
VIB8_AGRT5
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Best Local S
Matches 4
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P17798;
01-AUG-1990
01-NOV-1990
15-JUN-2002
                                                                               "The virB operon of Agrobacterium reading frames.";
                                                                                                                   MEDLINE=90318324; Pu
Kuldau G.A., de Vos
                                                                                                                                                                                                                                                                 Agrobacterium tumefaciens Plasmid pTiC58.
                                                                                                                                                                                                                                                                                                   VirB8 protein.
VIRB8 OR ATU6174 OR AGR_PTI_11.
SEQUENCE FROM N.A. MEDLINE-90301800;
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                        Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                       NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00382; AAA; 1.

PROSITE; PS00211; ABC_TRANSPORTER;

Hypothetical protein; Transport; II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
Pfam; Pr00005; ABC_tran; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
Science 282:754-759(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stephens R.S., Kalman S., I
Mitchell W.P., Olinger L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=D/UW-3/Cx; STRAIN=99000809; MEDLINE=99000809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
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                                                            Gen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute.
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FOR A METAL. PROBABLY RESPONSIBLE FOR ENER
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SWISS-POT entry is copyright. It is prouve. the Employers the Swiss Institute of Bioinformatics and the Employers the Swiss Institute. There are no restrictions in institute. There are no restrictions in a sit content is in managed by and for company to the children of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 AA;
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(Rel. 16, Last seq.
(Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39
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Kalman S., Lammel C.
                                                       221:256-266(1990)
                                                                                                                                       PubMed=2370849;
PubMed=2194232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46
26193 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                     0wen
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                                                                                                                                                                                                                                         alpha subdivision; Rhizobiaceae
                                                                                                                                                                                                                                                                                  (strain C58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inner membrane-associated (Potential)
                                                                                                                                                                                                                                                                                                                                                                    sequence'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL).
: DE74774507950365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                   McCaffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inner membrane; ATP-binding;
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                                                                                                tumefaciens
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                                                                                                                                                                                                                                                                                                                                                                    update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                237
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                                                                                                                                                                                                                                                                                                                                              update;
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ENERGY COUPLING TO THE
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                                                                                              Zambryski P.;
DTiC58 encodes
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Q., Koonin E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
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    BURGAR
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Best Local
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                 16-OCT-2001
16-OCT-2001
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                       EMBL; X53264; CAA37361.1; -.
EMBL; J03320; AAA91598.1; -.
EMBL; AE009436; AAL46410.1; -.
EMBL; AE007923; AAK90936.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;
                                                                                              SCHGR
                                                                                                                                                                                                                                                                                                         Crown gall tumor; Plasmid; CONFLICT 21 22
                                                                                                                                                                                                                                                                                                                                             PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.lsb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rogowsky P.M., Powell B.S., Shirasu K., Lin T.-S., Morel P., Zyprian E.M., Steck T.R., Kado C.I.;
"Molecular characterization of the vir regulon of Agrobacterium
                                                              PBCB_SCHGR
P82886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumefaciens: complete nucleotide sequence and gene
the 28.63-kbp regulon cloned as a single unit.";
Plasmid 23:85-106(1990).
    Putative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                          111 SYDA 114
                                                                                                                                                                                      1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: VIRB PROTEINS ARE SUGGESTED TO SURFACE AND THERE PLAY AN IMPORTANT ROLE TRANSFER TO PLANT CELLS.
                                                                                                                                                                                                                                                                                                                                            S12348;
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                                                                                                                                                                                                                                    Similarity
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   beta-carotene
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237
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                 (Rel. 40, Created)
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(Rel. 41, Last ann
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                                                                               STANDARD;
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129 S
; 26294 MW;
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Last sequence update)
Last annotation update
e binding protein.
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SA -> TR (IN REF. 2)
                                                                                                                                                                                                                                  Score 21; DB 1;
Pred. No. 2e+02;
                                                                              PRT;
                                                                                                                                                                                                                                                                                 71FEE1084B9597E9
                                                                                                                                                                                                                  Mismatches
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               update)
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                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                               MEDLINE-98332770; PubMed-9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S
McDonald L., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Purification and sequence determination of a yellow protein from sexually mature males of the desert locust, Schistocerca gregaria. Insect Blochem. Mol. Biol. 31:1183-1189(2001).

-!- FUNCTION: Has beta-carotene-binding activity. May be involved.
                                                                                                                                   This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                            spirochete.";
Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O83633;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazóa; Arthropoda; Mandibulata; Pancrustacea; Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Orthodomorpha; Acridoldea; Acridoldea; Cyrtacanthacridinae; Schistocerca.
                                                                                                                                                                                                                                                                                                                                                    STRAIN-Nichols;
                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                       Treponema
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wybrandt G.B., Andersen S.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Cuticle;
MEDLINE=21468012; PubMed=11583931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7010;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001
16-0CT-2001
                                                                                                                                                                                                                     "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                         /enter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 SYDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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Spirochaetales;
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(Rel. 40, Last annotation updat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E6074CF88D822EB5 CRC64;
                                                                                                                                                  ght. It is produced through Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DВ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hexapoda;
Caelifera;
                                                                                                                                                      a collaboration -
                                                                                                                                                                                                                                                                 Garland S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of male
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EMBL; AE001237; AAC65604.1; TIGR; TP0625; -.

Hypothetical protein; DOMAIN 165 208

28874 MW;

Coiled

coil; Complete proteome.
COILED COIL (POTENTIAL).
; 107002FE47B25186 CRC64;

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                                                                                                                                                                                                                                                                                                                                  RA Wood V. Gwilliam R. Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones L., Jones N., Leather S., Miblett D., Odell C.,
RA Oliver K., O'Nell S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Goffeau A., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Daga R.R., Cruzado L., Berkel M., Pettskin J.,
RA Spakers M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Taylor K., Langer M., Berkel M., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 35
RL7C_SCHPO
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Best Local S
Matches 4
                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for cor
                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                 Pfam; PF00327; Ribosomal_L30; 1.
TIGRFAMS; TIGR01310; L7; 1.
PROSITE; PS00634; RIBOSOMAL_L30; 1.
Ribosomal protein; Multigene family
                                                                                                                                                                      entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence u)
15-JUN-2002 (Rel. 41, Last annotation
60s ribosomal protein L7-C.
RPL7C OR SPBC18H10.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O60143;
15-DEC-1998
                                                                                                                            EMBL; AL022304; CAA18409.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4896;
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                                                                                                             nterPro;
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protein; Multigene
251 AA; 28730 MW;
                                                                                                          IPR000517; Ribosomal_L30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
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llarity 100.0%;
Conservative 0
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  MW;
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                      family.
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Pred. No. 2.1e+02;
  5382A27E39F3800E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                 a collaboration
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RESULT 36
SOJ_TREPA
 AC DT DT DT OC OC
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                                                                                                                                 RESULT 37
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Best Local
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                                                                           BIOC_SERMA
P36571;
01-JUN-1994
                                                                                                                                                                                                                                                                                 NP_BIND
SEQUENCE
                           BIOC
                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Dodson R., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Sodergren E., Hardham J.M., McLeod M.P., Salzberg M., Utterback T., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artlach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weldman J., Smith H.O.,
                                                   01-JUN-1994
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                      Biotin
                                                                                                                                                                                                                                                                                                                      InterPro; IPR000707;
Pfam; PF00991; ParA;
                                                                                                                                                                                                                                                                                                                                                EMBL; AE001208; AAC65260.1; -. TIGR; TP0272; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence spirochete.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
             Serratia marcescens
                                                                                                                                                                                                                                                                                                        ATP-binding; Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein soj
                                                                                                                                                                           228 SYDA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 SYDA 61
                                                                                                                                                                                                  1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TREPA
                                                                                                                                                                                                                                                                                                                                               TP0272;
                                      synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J.C.
                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
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                                                                                                                                                                                                                                          Similarity
Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                               10
253 ‡
                                   (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 41, Last annotation updathesis protein bioC.
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17 AT
27341 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spirochaetaceae; Treponema
                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                               ATP (POTENTIAL).
; 284B3B31A9306EDA CRC64;
                                                                                                                                                                                                                                         Score 21; DB 1;
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21; DB 1;
Pred, No. 2.1e+02;
                                                                                                                                                                                                                              Mismatches
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                                                   update)
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 Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration
                                                                                                                                                                                                                            0;
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RESULT 38
CAH2_CHICK
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P077630;
P077630;
P077630;
P0787630;
P
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                                                                                                                                                                                                                                                                                                   Mezquita J., Pau M., Mezquita C.;

"A novel carbonic anhydrase II mRNA isolated from mature chicken testis displays a TATA box and other promoter sequences in a leady untranslated region not present in somatic tissues.";

Gene 147:231-235(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biotin biosynthesis;
SEQUENCE 255 AA;
SEQUENCE OF 4-259 FROM N.A. STRAIN-White leghorn; TISSUE-Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Hubbard White Mountain; TI MEDLINE-95011620; PubMed=7926806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D17468; BAA04287.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appl Environ. Microbiol. 59:3225-3232(1993).
1- FUNCTION: BIOC IS INVOLVED IN AN EARLY, BUT CHEMICALLY UNEXPLORED,
STEP IN THE CONVERSION OF PIMELIC ACID TO BIOTIN.
-1- PATHWAY: Biotin biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain.
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                                                                                                                                                                                            STRAIN=White leghorn; MEDLINE=87146391; PubMed=3029691;
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01209; Ubie_methyltran;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000051; SAM_bind.
InterPro; IPR004033; UbiE/COQ5_Metrf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=615;
                                                                                                                                   Yoshihara C.M., Lee J.-D., Dodgson J.B., "The chicken carbonic anhydrase II gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sakurai N., Imai Y., Masuda M., Komatsubara S., Molecular breeding of a biotin-hyperproducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SYDA 4
                                                                                                                intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE METHYLTRANSFERASE SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYDA
                                                                                    on position.";
Acids Res. 15:753-770(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Eute
Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase; Methyltransferase
27776 MW; 1DD2532B3FCA7F67 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.2e+02;
hes 0;
                                                                                                                                      evidence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dehydratase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serratia marcescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tosa
                                                                                                                                         for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                      recent shift
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               II)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CA-II)
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В
                                       Q
                                                                                                                                                                            A FIGURE A REPLANTA REPLANTA CON PROPOSORIA DE CONTROL REPLANTA RE
                                                                                      Matches
                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 214957; CAA78681.1; EMBL; X12639; CAA31175.1; EMBL; X06000; CAA29417.1; EMBL; X06001; CAA29417.1; J EMBL; X06002; CAA29417.1; J EMBL; X06003; CAA29417.1; J EMBL; X06004; CAA29417.1; J EMBL; X06005; CAA29417.1; J EMBL; X06005; CAA29417.1; J EMBL; X06005; CAA29417.1; J EMBL; X06005; CAA29417.1; J EMBL; X04810; CAA28501.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X17378; CAA35250.1; -
EMBL; M25943; AAA48646.1; -
PIR; S01078; S01078.
PIR; A26415; A26415.
PIR; S10229; S10229.
PIR; S10229; S10229.
PIR; S31987; S31987.
                                                                                                                                                                                                 CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90192090; PubMed-1969140; Godbout R., Andison R., Upton C., Day R.; "Utilization of the second polyadenylation the chicken carbonic anhydrase II gene."; Nucleic Acids Res. 18:1049-1049(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yoshihara C.M., Federspiel M., Dodgson J.B.;
"Isolation of the chicken carbonic anhydrase II gene.";
Ann. N.Y. Acad. Sci. 429:332-334(1984).
-i- FUNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE.
-i- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
-i- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                               METAL
METAL
                                                                                                                                                                                                                                                                                                                                                            Lyase; Z
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00194; carb_anhydrase; ProDom; PD000865; Euk_COanhd;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=84255154; PubMed=6331256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 7-86 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 221-259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence of carbonic anhydrase II cDNA from chick retina."; Eur. J. Biochem. 162:119-122(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rogers J.H.
                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=87133522; PubMed=3102231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
49
                                          1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produ
ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS
SYDA
                                                                                                           Similarity
52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001148; Euk_COanhd
                                                                                                                                                                            249
259 AA;
                                                                                                                                                                                                                                                0
93
95
118
4
7
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      EUK_CO2_ANHYDRASE;
                                                                                                                                                                                                 93
93
118
118
7
86
                                                                                                                                                                            28876
                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED.
JOINED.
JOINED.
JOINED.
                                                                                                                                                                                               ZINC (CATALYTIC).
ZINC (CATALYTIC).
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ZINC (CATALYTIC).

W -> L (IN REF. 3).
D -> G (IN REF. 5).
V -> V (IN REF. 5).
                                                                                      0,
                                                                                                           Score
Pred.
                                                                                                                                                                               DF133083864A4969
                                                                                        Mismatches
                                                                                                           No.
                                                                                      2.2e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no
                                                                                                                                  DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            signal at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and the
                                                                                                                                Length 259
                                                                                                                                                                               CRC64;
                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restrictions
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                                                                                    Gaps
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RESULT

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RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooljman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Bernelser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Clark L., Doggett J., Cronin A., Quail M., Bray-Allen S.,
RA Pettett A., Rajandream M.A., Lyne M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Lennard N., McLay K., Mayes R.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Heijnen L., Schwarz S., Scholler E., Johnson S., Tacon D., Jesse T.,
RA Giraria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Schnon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Schon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Minx P., Bentley D., Fulton B., Miller N., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Manned J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Martial D., Berghoff A., Jones K., Dothe K., Cotton M., Joshu C.,
RA Manned S., Shohdy N., Stang C., Sun H., Lamar B., Yordan C.,
Schon M., Martianssen R., McComble W.R.,
Theliana J., Till S.,
Thaliana J., Martianssen R., McComble W.R.,
Theliana J., Till S.,
Thaliana J., Johnson A., McComble W.R.,
STRAIN-cv. Col
Shinozaki K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F., Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., Braeken M., Welljens I., Voet M., Bastiaens I., Aert R., Defoor E., Weltzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Weltzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
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                                                                                                                                                                                                                                                                                                                                            Nature
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosidispermatophyta; Magnoliophyta; eudicotyledons; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Expansin-like 2 precursor (At-EXPL2) (Ath-ExpBeta-2.2).
EXPL2 OR AT4G38400 OR F22II3.170.
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MEDLINE=20083488; Pu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9SVE5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXL2_ARATH
                                                                                                                                                                                                                                                                                                                                      402:769-777(1999).
                                                                                                                                                                                                                                            Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10617198;
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                                                                                                                                                     Theologis A.;
lones (RAFLS) sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Terryn N.,
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RESULT 40
FLIP_CAUCR
ID FLIP_C
AC Q45980
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                          FLIP_CAUCR STANDAKU; Q45980; Q45980; Q1-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence up 15-JUN-2002 (Rel. 41, Last annotation figure 15-JUN-2002 (Rel. 41) Last annotation flip.
Nierman W.C., Feidblyum T.V., Laub M.T., Paulsen I.T., Nelson K Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., E DeBoy R.T., Dodson R.J., burkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Wh
                                                                                                                                                     Caulobacter crescentus division.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein;
SIGNAL
CHAIN 2
                                                                     MEDLINE=21173698;
Nierman W.C., Felo
                                                                                                                                                   division.
                                                                                                                                                                                          Wingrove
                                                                                                                                                                                                   Gober J.W.,
                                                                                                                                                                                                                                STRAIN-ATCC
                                                                                                                                                                             "Temporal and
                                                                                                                                                                                                               MEDLINE=95325304; PubMed=7601828;
                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha
                                                                                                                                                                                                                                                                                                         Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                    NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPRO00882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen; 1.
PRINTS; PR01225; EXPANSYBAMLY.
ProDom; PD012179; Pollen_allergen; 1.
PROSITE; PS50843; EXPANSIN_CBD; 1.
PROSITE; PS50843; EXPANSIN_CBD; 1.
PROSITE; PS50843; EXPANSIN_EG45; 1.|
Glycoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL035539; CAB37496.1;
EMBL; AL161593; CAB80505.1;
EMBL; AV050470; AAK91483.1;
EMBL; AF378855; AAK55658.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF378855; AAK! HSSP; P43214; 1WHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not 'removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SYDA 244
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                                                                                                                                      Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SYDA 4
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                                                                                                                                                                                                                                                                                                                      OR CC0951
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                                                                                                           FROM
                                                                                                                                                                                                                             FROM N.A.
TCC 19089 /
                                                                                                                                                                                        J.A.;
                                                                                                                                                                                                    Boyd C.H., Jarvis M.,
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22
42
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103
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                                                                                                                                   177:3656-3667(1995).
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                                                                                 PubMed=11259647;
                                                                                                / CB15;
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EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
N-LINKED (GICNAC. ..) (
N-LINKED (GLCNAC. ..)
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EXPANSIN-LIKE :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B57B4C921899F40D CRC64;
                                                                                                                                                                                                                                                                                       subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                               Mangan E.K., Rizzo M.F.,
                                                                                                                                                                                                                                                                                                                                                                                             266
                                                                                                                                                                                                                                                                                                                                         update)
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  Ermolaeva M., White O.
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Proc.

Salzberg

S.L.,

Venter J.C.,

Shapiro L., Fraser C.

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Best Local
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Q9X712;
16-OCT-2001
 "Complete
Submitted
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TRANSMEM
                                                                                                                                                                                                                   (Ketopantoate hydroxymethyltransferase PANB OR CGL0114.
                                                                                                                                                                                                                                                                                                                   CORGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                  SEQUENCE FROM N.A. STRAIN-ATCC 13032
                                                                             overproduction."
                                                                                      "D-Pantothenate synthesis in panBC and genes encoding L-va
                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 13032 / DSM
MEDLINE-99240418; PubMed
                                                                                                                                                                   Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                                                                           Actinomycetales; Corynebacterineae;
                                                                                                                                                                                                   Corynebacterium glutamicum Bacteria; Actinobacteria; F
                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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ProDom; PD002586; FliP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; CC0951;
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                                                                                                                                                                                                                                                                                                                                                                                     1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO THE FLIP/MOPC/SPAP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nplete genome sequence of Caulobacter crescentus.";

2. Natl. Acad. Sci. U.S.A. 98:4136-411(2001).

FUNCTION: MAY BE A COMPONENT OF THE FLAGELLUM. IT

NORMAL CELL DIVISION. MAY BE IMPLICATED IN THE SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIRULENCE FACTORS
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AE005772;
                                                                  Environ. Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 4; Conserv
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PS01061;
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                       S
genomic sequence of Corynebacterium (MAY-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR01103; flip; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                               Sahm H.;
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78
122
222
246
28527
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FLIP_2; 1.
                                                                                                                        / DSM 20300 / NO PubMed=10223988
                                DSM 20300 / NCIB 10025;
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                                                                                         L-valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete
                                                                                                                                                                                         m (Brevibacterium flavum).
Actinobacteria (class); Actin
cterineae; Corynebacteriaceae;
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Pred. No.
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hes 0;
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 glutamicum databases.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura Mosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S., Tabata S., "Sequence analysis of the genome of the unicellular cyanoba Synechocystis sp. strain PCC6803. II. Sequence determinatio entire genome and assignment of potential protein-coding representations of the property.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYNT_SYNY3
Q54735; P74088;
01-NOV-1997 (Re.
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EMBL; X96580; CAA65397.1; ...
EMBL; AP005274; BAB97507.1; ...
EMBL; AP005274; BAB97507.1; ...
InterPro; IPR03700; Pantoate_transf.
Pfam; PF02548; Pantoate_transf; 1.
IIGRFAMS; TIGR00222; panB; 1.
IIGRFAMS; TIGR0022; panB; 1.
IIG
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So A.K.C., Espie G.S
Submitted (MAR-1996)
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01-NOV-1997 (Rel. 35, Last seq
16-OCT-2001 (Rel. 40, Last ann
Carbonic anhydrase (EC 4.2.1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechocystis sp. (strain Bacteria; Cyanobacteria; C
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                                                                                                                                                                                                                                                                                                                                                                        FÜNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE. TO PHOTOSYNTHETIC CARBON DIOXIDE FIXATION. CAPTALYTIC ACTIVITY: H(2)C(3) = CO(2) + H(2)C. SIMILARITY: BELONGS TO THE PLANT AND PROKARYOTIC CAPTAINLY AND PROKARYOTIC CAPTAINLY BELONGS TO THE PLANT AND PROKARYOTIC PROTECTE PLAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate +
                                                                                                                                                                                                                                                                                                                                               ANHYDRASE FAMILY.
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Pred. No. 2.3
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T AND PROKARYOTIC CARBONIC
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PROSITE; PS00704; PROK_CO2_ANHYDRASE_1; 1

PROSITE; PS00705; PROK_CO2_ANHYDRASE_2; 1

Lyase; Zinc; Complete proteome.
CONFLICT 219 219

SEQUENCE 274 AA; 30761 MW; 2F4F634246C0
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Rhabditidae; Pelode
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                           SEQUENCE
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MEDILINE-98037514; PubMed=9371463; |

A Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J.,

A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

A Harrison D., Hoang L., Keagle P., Jumm W., Pothier B., Qiu D.,

A Harrison D., Hoang L., Keagle P., Jumm W., Pothier B., Qiu D.,

A Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

Jiwani N., Caruso A., Bush D., Safer H., Pattwell D., Prabhakar S.,

A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

A Daniels C.J., Mao J.-I., Rice P., Nolling J., Remoautotrophicum

"Complete genome sequence of Methanobacterium thermoautotrophicum

"Complete G.J., Mao J.-I., Rice P., Nolling J., Remoautotrophicum

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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
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Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermopacter.
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Pfam; PF00459; inositol_P; 1.

PROSITE; PS00629; IMP_1; 1.

PROSITE; PS00630; IMP_2; 1.

PROSITE; PS00630; IMP_2; 1.

Hydrolase; Magnesium; Complete proteome.

Hydrolase; Magnesium; Complete POAE435970AED882 CRC64;

SEQUENCE 280 AA; 30173 MW; F0AE435970AED882 CRC64;
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P32436;
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                        Bacillus subtilis.
Bacteria; Firmicutes;
NCBI_TaxID=1423;
MEDLINE=94018599; PubMed=8412657;
                                                                                                       SEQUENCE FROM N.A.
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Pred. No. 2.4e+02;
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RX MEDLINE-98044033; PubMed-9384377;

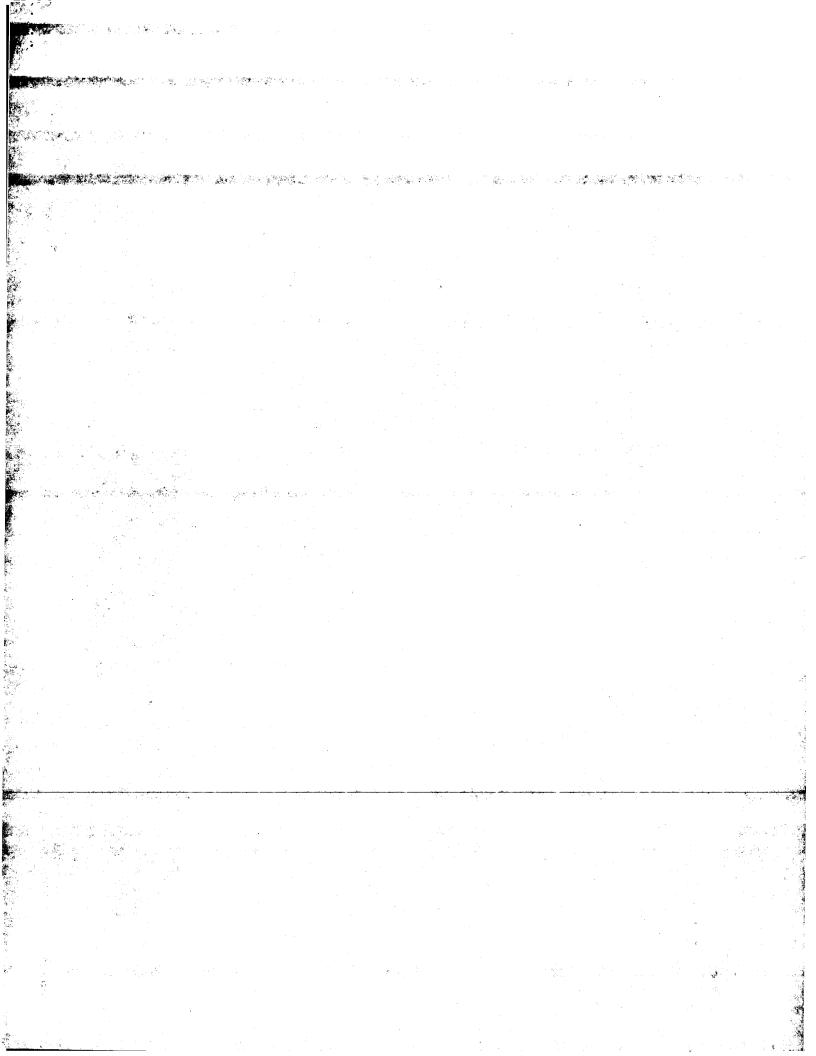
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RA Azevedo V., Bertero M.G., Messieres P., Bolotin A., Borchert S., RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., RA Azevedo V., Bertero M.G., Brans A., Braun M., Brignell S.C., Bron S., RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D., RA Britar K.D., Errington J., Fabret C., Ferrari E., Foulger D., RA Brits C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., RA Hilbert H., Holsappel S., Hosono S., Klaerr-Blanchard M., Klein C., RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Klein C., Kochter P., Koningstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., RA Mediaue C., Medique C., RA Mediaue C., Medique C., RA Parro V., Pohl T.M., Ogawa K., Ogiwara A., Oudega B., Park S.H., RA Parro V., Pohl T.M., Ogawa K., Ogiwara A., Oudega B., Park S.H., RA Parro V., Pohl T.M., Portetelle B., Rapoport G., Rey M., Reynolds S., Ra Prescant E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Ra Prescant E., Schleich S., Schroeter R., Scoffone F., RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Ra Raynotto M., Walat A., Yananoto M., Vannier F., Vassarotti A., RA Viati A., Walat A., Yananoto H., Yamane K., Yasamoto K., Yata Y., Yat
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                                                                                         EMBL; Z18629; CAA79225.1; -.
EMBL; U56901; AAC44939.1; -.
EMBL; 299122; CAB15565.1; -.
EMBL; M23558; -; NOT_ANNOTATED_CDS
PIR; D30191; D30191.
PIR; S28596; S28596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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J. Bacteriol. 170:5102-5109(198).
-i- SIMILARITY: TO S. AUREUS PLASMID PSK1 HYPOTHETICAL 15.5 kDa PROTEIN (AC P13977) AND TO M.GENITALIUM MG326.
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"Sequence of the Bacillus
to 307 degree.";
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Search completed: February 6, 2003, 11:16:46
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Copyright (c) 1993 - 2003 Compugen Ltd.
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               OByyx6 anabaena sp
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Q9NFH5; Q9NFH5; 2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
101-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 4.8 kDa protein (Fragment).
Plasmodium falciparum (Isolate 3D7).
Plasmodium falciparum (Isolate 3D7).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Q8YYX6 PRELIMINARY; PRT;
Q8YYX6;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
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Spielmann T., Beck H.P.;
'Analysis of stage-specific transcription in Plasmodium falciparum reveals set of genes exclusively transcribed in ring stage parasites.";
Mol. Biochem. Parasitol. 111:453-458(2000).
EMBL; AJ290921; CAB92930.1; -.
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Q9X374 PRELIMINARY;
Q9X374;
01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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Q12081;
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EMBL; M15168; AAA66931.1; --
EMBL; M15167; AAA66930.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87120291; PubMed=3027892; Parikh V.S., Morgan M.M., Scott R., Clements L.S., Butow R.A.; The mitochondrial genotype can influence nuclear gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein (Fragment).
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
EMBL; AP003583; BAB72673.1; -
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
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6029 MW; 42F9CC5A554CFF40 CRC64;
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MEDLINE-21470413; PubMed-11586369;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

A Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

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Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

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"Genome sequence of Yersinia pestis, the causative agent of plague.";

Nature 413:523-527(2001).

R EMBL, ALI17211; CAB62375.1;

R EMBL, ALI17211; CAB62375.1;

R Hypothetical protein; Plasmid; Complete proteome.

SEQUENCE 75 AA; 8293 MW; C6C26AEC212F2ABF CRC64;
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Q9RIC5;
Q1-MAY-2000
Q1-MAY-2000
Q1-MAR-2002
Q9MC41
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Okinaka R.T., Cloud K., Hampton O., | Hoffmaster A.R., Hill K.K.,
Keim P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter I
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"Sequence and organization of pXO1, the large Bacillus anthracis
plasmid harboring the anthrax toxin genes.";
J. Bacteriol. 181:6509-6515(1999). |
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
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Bacillus anthracis.
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(TrEMBLrel. 20, Last annotation update)
1 protein YPMT1.68A.
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01-OCT-2000
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Q9Z3S8;
Q1-MAY-1999
                                                                        MEDLINE=97080503; PubMed=8921848;
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EMBL: AJ224510; CAB37318.1; -. InterPro; IPR001126; UMUC_like.
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"Sequence of the Genome of the Temperate,
Pseudomonas aeruginosa Bacteriophage D3.";
J. Bacteriol. 182:6066-6074(2000).
EMBL; AF165214; AAF80767.1; -.
SEQUENCE 77 AA; 8266 MW; 39DAE91077F72
                                                                                                                                                                                                                                                                              "Replication regions from plant plasmids are similar to ColE2-r Microbiology 145:325-334(1999).
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Vivian A., Murillo J.;
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Bacteria; Prote
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Baguero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget (
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson I
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Maddeno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell I
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vasquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Comparative genomics of Listeria species.";
Science 294.849-852(2001).
EMBL; AL596173; CAC98075.1; -.
Listilist; LIN02849; -.
Hypothetical protein; Complete proteome.
SEQUENCE 80 AA; 9908 MW; B625A9DF7CF7CAD6 CRC64;
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Lindler L.E., Plano G.V., Burland
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MEDLINE=21537279; PubMed=11679669;
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                                                                                                                                                                                          NCBI_TaxID=1639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
SEQUENCE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001126; UN Pfam; PF00817; IMS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Plant Pathol. EMBL; AJ251482; CA
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Hypothetical protein;
CROHENCE 81 AA; 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-RACE 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arnold D.L., Jackson R.W., "Evidence for the mobility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9K510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=59510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete DNA sequence and detailed KIM5 plasmid encoding murine toxin a Infect Immun. 66:5731-5742(1998). EMBL; AF074611; AAC82735.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 SYDA 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SYDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome
          E., Dominguez-Bernal G., K.-D., Fsihi H., Garcia-
P., Frangeul L., Buchrieser C., Rusniok C., Amend A., F., Berche P., Bloecker H., Brandt P., Chakraborty T. A., Chetouani F., Couve E., de Daruvar A., Dehoux P., E., Dominguez-Bernal G., Duchaud E., Durant L., Dussur K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 4; Conserv
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4; Conser
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2 (TrEMBLrel. 20, L
2 (TrEMBLrel. 20, L
11 protein lmo2701.
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Conservative
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                                                                                                                                                                                                                     Bacillus/Clostridium group; Bacillales;
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gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                          Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0EFD90A9398DDF3F CRC64;
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Pred. No.
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aces of Pseudomonas syringae pv.
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RA BORKOVA D., BOLLIAI, M.N., CAMLEY H., Cadieu E., Center A., CHALLEY H., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Deng Z., Mays A.D., Dew I. Dietz S.M., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dorbin K.J., Evangelista C.C., Ferriaz C., Ferriar S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Hostin D., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lais Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Vencer E., Wang A.H., Wang X., "Pan R., Venter E., Wang A.H., Wang X., "P
                 ACCOCCARACTOR AC
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Q9VQT7
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Butter H., Caddeu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Bahler H., Caddeu E., Center A., Chandra I.,
Charve T. M. Camiley C. Dahler C. Inavency I. R. Davies D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09VQT7;
01-MAY-2000
01-MAY-2000
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Drosophila melanogaster (Fruit fly).

Mrharoa: Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Comparative genomics of Listeria Science 294:849-852(2001).
EMBL, AL591984, CAD00914.1; -.
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Neoptera; Endopterygota; Dip
a; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Last sequence up
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Pred. No. 5.7
0; Mismatches
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C94155A9DB68BAFB CRC64;
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RESULT 14
Q8X8N9
ID Q8X8N
AC Q8X8N
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
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Q8ZQ21
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EMBL; AE003579; AAF51077.1; -. HSSP; P02760; IBIK.

Flybase; FBgn0031560; CG16713.
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI.
PFAMP; PR000759; BASTICPTASE.
RODOM; PD000222; Kunitz_BPTI; 1.
REMART: SM00131; KU; 1.
               O8X8N9 PRELIMINARY;
Q8X8N9;
O1-MAR-2002 (TrEMBLrel. 2
O1-MAR-2002 (TrEMBLrel. 2
O1-MAR-2002 (TrEMBLrel. 2
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Q8ZQ21;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                            Nature 413:852-856(2001).

EMBL; AE008750; AAL20091.1; -.

Hypothetical protecin; Complete proteome.

SEQUENCE 84 AA; 9717 MW; 078AF3C835A3342F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
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PROSITE; PS50279; BPTI_KUNITZ_2; 1.
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Pred. No. 5.9
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nu S., Zhu
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RESULT
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Best Local
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"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Reeves C.D., Soliday C.L.;

Sequence of Streptomyces roseofulvus containing genes for fremolicin biosynthesis.";

Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF058302; AAC18105.1;

InterPro; IPR003880; Ppantne_attach.

Pfam; PF00550; pp-binding; 1.

PROSITE; PS50075; ACP_DOMAIN; 1.
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01-AUG-1998
01-MAR-2002
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MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli

0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                 Streptomyces genes probably encoding antibiotic frenolicin.";
Gene 142:31-39(1994).
[2]
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MEDLINE-94237486; PubMed-8181754;
Bibb M.J., Sherman D.H., Omura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces roseofulvus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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MEDLINE=21074935; PubMed=11206551;
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Escherichia coli 0157:H7.
Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                                                                         Bibb M.J., Sherman D.H., Omura S., Hopwood D.A.; "Cloning, sequencing and deduced functions of a cl Streptomyces genes probably encoding biosynthesis
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Pred. No.
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RESULT 17
Q9GY45
ID Q9GY4
AC Q9GY4
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AC DT 01-06
DT 01-07
DE HYPOT
GN LM15
GN LLeist
OC Eukar
OC Eukar
OC NCBI
RN [1]
RN [1]
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RR SEQUE
RC STRAJ
RA MULPEN
RA OLIVE
RA SUDMI
DR EMBL;
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DR EMBL;
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Murphy L., vuc...

Oliver K.;

Oliver K.;

Submitted (AUG-2001) to the Submitted;

Submitted; CAC02005.2

(EMBL; AL390114; CAC02005.2
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Q827L4;
01-MAR-2002
01-MAR-2002
                                                                                                         STRAIN-FRIEDLIN;
Murphy T
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STY1199.
Salmonella typhi
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Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                             Hypothetical LM12.105.
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01-OCT-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Hypothetical predicted p
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01-MAR-2001
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SEQUENCE 85
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Q91Z41;
01-DEC-2001
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SEQUENCE
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                       Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; BC010220; AAH10220.1; -. InterPro; IPR002005; Rab_GDI_REP. | Pfam; PF00996; GDI; 1.
                                                            Strausberg
                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                          Hypothetical 10.5 kDa protein
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01-DEC-2001 (TREMBLIE 119,
01-JUN-2002 (TREMBLIE 21,
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NCBI_TaxID=10566;
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PRINTS; PR00111; ABHYDROLASE.
SEQUENCE 87 AA; 9449 MW; 7F983D4
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                                                                                                                  Mus musculus (Mouse)
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STRAIN-HPVX24
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Sciurognathi; Muridae;
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Murinae; Mus
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RESULT
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 10.5 kDa protein.
0RF392.
                                                                                        STRAIN-GMI1000;
STRAIN-GMI1000;
STRAIN-STRAIN-GMI1000;
Salamoubat M., Genin S., Artiquenave F., Gouzy J., Mangenot Salamoubat M., Genin S., Brottier P., Camus J.C., Cattolico L. Arlat M., Billault A., Brottier P., Camus J.C., Cunnac S., Deman Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Welssenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearu Nature 415:497-502(2002).
EMBL; AL646062; CAD14830.1; -.
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01-NOV-1998
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"Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromaticivorans strain F199.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF079317; AAD03892.1;
Hypothetical protein; Plasmid.
SEQUENCE 95 AA; 10535 MW; AC530A9B1563B46D CRC64;
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Bacteria: Proteobacteria; beta subdivision; Ralstonia
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                                          Hypothetical protein; Complete SEQUENCE 96 AA; 10601 MW; 9
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57 SYDA 60
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Pred. No. 6.6e+02;
Pred. No. 6.6e+02;
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01-JAN-1998
01-JAN-1998
01-DEC-2001
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Jang Y.-J., YOO H.-S.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ
EMBL; U97365; AAB63857.1; -.
InterPro; IPR000517; Ribosomal_L30.
InterPro; IPR000517; Ribosomal_L30; 1.
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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SEQUENCE
                                                                                                  STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa (japonica cultivar-group) genomic DNA, chromosome clone:B1142C05.";
                                                        Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003410; BAB89131.1; -. SEQUENCE 100 AA; 11168 MW; 0E721D6E0EC06CAA CRC64;
                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                 B1142C05.31 protein.
B1142C05.31.
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Schizosaccharomycetales; Schizosaccharomycetaceae;
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60S ribosomal protein L7B
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O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 11.4 kDa protein.
ORF680.
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STRAIN-ATCC 25586;

MEDLINE-21886394; PubMed=11889109;

Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis & Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.;

"Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586."

J. Bacteriol. 184:2005-2018(2002).

EMBL; AE010519; AAL94251.1; ".
                                                                                                      Romine M.F., Stillwell L.C., Wong K.-K., Thurston S.J., Sensen C.W., Gaasterland T., Saffer J.D., Fredrickson J. "Complete sequence of a 184 kb catabolic plasmid from Sparomaticivorans strain F199.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AF079317; AAD03931.1; -
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                                                                                                                                                                                                                             Bacteria; Proteobacteria; Novosphingobium.
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                                                                                                                                                                                                                 NCBI_TaxID=48935;
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                                  Local Similarity
les 4; Conserv
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SYDA 4
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103 AA; 11444 MW;
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ilarity 100.0%;
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1550 мw; 0A65A09071054742
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Fusobacterium
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01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                Complete
SEQUENCE
                                                                     MEDLINE-20504483; PubMed-11016950; Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Rieby M., Hood L., DasSarma S.; "Genome Sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S.,
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., Whi
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                     Halobacterium sp. (strain NRC-1). |
Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE006484; AAK33252.1; -. Hypothetical protein; Complete SEQUENCE 106 AA; 12466 MW;
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STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
MEDLINE=21192684; PubMed=11296296;
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NCBI_TaxID=1314;
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(TrEMBLrel. 19, Last annotation)
100.0%;
llarity 100.0%;
Conservative 0
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16,
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          Score 21;
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0743A62E08B19951 CRC64;
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Q8W5F8;
Q1-MAR-2002
Q1-MAR-2002
Q1-JUN-2002
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Q942U5;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2002
          STRAIN-CV.
Sasaki T.,
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 10 BAC OSJNBa0073L20 genomic sequence.";
Submitted (APR-2022) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N., Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbu: Salzberg S.L., White O., Fraser C.M.;
"Oryza sativa chromosome 10 BAC OSJWHBD008A05 genomic sequence."
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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                            SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
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P0506E04.27.
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                                                                                                                                     Spermatophyta;
Ehrhartoideae;
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67 SYDA 70
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Q9XCB3;
01-NOV-1999
01-NOV-1999
SEQUENCE FROM N.A.
STRAIN-ITI 376;
Thorolfsdottir E.T.T., Backman V.M.,
Thorobjarnardottir S.H., Palsdottir A
Kristjansdottir S., Eggertsson G.;
                                                                                                                                                                                     OlYCB3;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
01-MAR-2002 (TremBLrel. 20, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, clone:p0506E04.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003272; BAB67949.1; -.
Interpro; IPR002086; Aldehyde_dehydr.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
SEQUENCE 111 AA; 11334 MW; 74AB4291D5334A2A CRC64;
                                                                                                                                    Rhodothermus marinus Bacteria; CFB group; NCBI_TaxID=29549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE L1P EMBL; AF247854; AAF77035.1; -. InterPro; IPR002143; Ribosomal_L1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis remanei.
Eukaryota; Metazoa; Nem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPL-10A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribosomal protein L1 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00687; Ribosomal_L1; 1.
PROSITE; PS01199; RIBOSOMAL_L1;
                                                                                                                                                                                                                                                                                                                                                              3
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112 AA;
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                                                                                                                                                         Rhodothermus
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Pred. No.
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RESULT 33
Q9RZP8
ID Q9RZP
AC Q9RZP
AC Q9RZP
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DT 01-JU
DE Salic
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Matches 4
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Q95WK3;
01-DEC-2001
01-DEC-2001
01-MAR-2002
                                               Bacteria; Thermus/Deinococcus Deinococcaceae; Deinococcus.
                                                                                              O9RZP8
O9RZP8; PRELIMINARY; PRT; 113 AA.
O9RZP8; O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Salicylate monooxygenase-related protein.
DRB0072.
 STRAIN-R1;
                                                                       Plasmid MP1
                                                                                Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                         **Krzywinski J., Wilkerson R.C., Besansky N.J.;
**Toward understanding Anophelinae (Diptera, Culi
Insights from nuclear single copy genes and the
Syst. Biol. 50:540-556(2001).
EMBL; AF317810; AAL18429.1;
Interpro; IRR001282; G6PD.
Pfam; PF00479; G6PD; 1.
            SEQUENCE FROM N.A.
                                   NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G6PD.
                                                                                                                                                                                                                                                                                                                                                                 Fram; PF004/9; G6PD; 1.
ProDom; PD001129; G6PD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pterygota;
Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anopheles pseudopunctipennis.
Eukaryota; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Heat shock in Rhodothermus marinus: Cloning and sequence analysis of the groESL, dnak and dnaJ genes.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF145250; AAD37972.1; -
InterPro; IPR00293; Methyltransf_3.
Pfam; PF01596; Methyltransf_3; 1.
Methyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=46955;
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113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
hosphate dehydrogenase (Fragment).
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                                                                                                                                                                                                                                                                               100.0%; ilarity 100.0%; Conservative 0;
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13423 MW;
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Endopterygota; Diptera; Nematocera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                          Score 21; DB 5; Pred. No. 8.2e+02; Charletones 0;
                                                        group;
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Pred. No.
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                                                        Deinococci;
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s 0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Culicidae) phylogeny: the weight of evidence.";
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                                                         Deinococcales;
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RESULT 35
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Q8RSN6
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                                           Q92J33
Q92J33;
Q1-DEC-2001
Q1-DEC-2001
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                     Q8RSN6;
Q8RSN6;
Q1-JUN-2002
Q1-JUN-2002
Q1-JUN-2002
           Rickettsia
                                   Hypothetical
   Bacteria;
                                                                                                                                                                                                                                                          system of the RND-MFP-OEP type conferring erythromycin a roxithromycin resistance in Pseudomonas sp. B13."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AJ431260; CAD24324.1; -.
                                                                                                                                                                                                                                                                                                                                                                          uncultured bacterium.
Plasmid pB4
                                                                                                                                                                                                                                                                                                                                                                                                  Upf54.8 protein. UPF54.8.
                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               Bacteria; environmental samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White O., Elsen J.A., Heldelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                       Plasmid.
                                                                                                                                                                                                                                                                                                           "The IncP
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=77133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monooxygenase; Plas
SEQUENCE 113 AA;
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InterPro; IPR003042; Rng_mnoxygenase.
Pfam; Pf01360; Monooxygenase; 1.
PRINTS; PR00420; RNGMNOXGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE001826; AAF12594.1; -.
TIGR; DRB0072; -.
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4; Conservative
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                                                                                                                                                                                                                                                                                         beta plasmid pB4 encodes a tripartite antibio
 Proteobacteria;
              conorii.
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(TrEMBLrel.)
                                             (TrEMBLrel. 19,
(TrEMBLrel. 19,
(TrEMBLrel. 19,
                                                                                         PRELIMINARY;
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                                  protein
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                                  RC0236
 alpha
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Last annotation update)
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Pred. No.
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Pred. No. 8
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subdivision;
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                                          annotation update)
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hes 0;
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s 0;
Rickettsiales
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romycin and
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RESULT 37
Q92US
AC Q92US
AC Q92US
DT 01-DE
DT 01-JU
DE PUTAT
GN RH101
OS Rhizo
OG Plasm
OC Bacte
OC Rhizo
RN [1]
RP SEQUE
RX MEDL]
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Q991X7
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Best Local S
Matches 4
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Best Local :
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Q92US4;
Q92US4;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Q991X7;
Q1-JUN-2001
Q1-JUN-2001
Q1-DEC-2001
                                                                       Putative regulatory protein, arsk family. RB1016 OR SMB21576.
Rhizobium meliloti (Sinorhizobium meliloti). Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Samson D., Roux V.,
Raoult D.;
                                                         Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                  "Novel and diverse integron-like gene cassette natural environments.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ EMBL, AF349050; AAK28563.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Stokes H.W., Nield B.S., Gillings M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uncultured organism.
unclassified; enviro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat)
Hypothetical 12.8 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mechanisms of evolution in Rickettsia conorii a Science 293:2093-2098(2001). Science 293:2093-2098(2001). Hypothetical protein; Complete proteome. SeQUENCE 115 AA; 13298 MW; C419CB796D5BD8A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-MALISH 7;
MEDLINE-21442074; PubMed-11557893;
STRAIN=1021;
MEDLINE=21396508; PubMed=11481431;
                                                                                                                                                                                                                                                                                                                                                               Hypothetical SEQUENCE 1:
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NCBI_TaxID=781;
                            SEQUENCE FROM N.A
                                                   NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=155900;
                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                       Local Similarity
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116 AA;
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Cossart P., Weissenbach
                                                                                                                                                                                                                                                                                                                                                            12765 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in Rickettsia conorii and
                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                         Score 21; DB Pred. No. 8.4); Mismatches
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Pred. No. 8.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rickettsia.
                                                                                                                                                                                                                                                                                                                                                            D92EC331445B2BB6
                                                                          subdivision; Rhizobiaceae group;
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Q9XVL0
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Best Local (
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Q9XVL0;
01-NOV-1999
SEQUENCE FROM N.A. MEDLINE=97061201; PubMed=8905231; Kaneko T., Sato S., Kotani H., Ta
                                                                                P73361;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Hypothetical protein slr1210.
                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                       Synechocystis sp. (strain
Bacteria; Cyanobacteria;
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81101; CAB03198.1; -.
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01-NOV-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001845; HTH_Arsr.
Pfam; PF01022; HTH_5; 1.
Plasmid; Hypothetical protein;
SEQUENCE 121 AA; 12870 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti."; proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
EMBL; AL603645; CAC49416.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Finan T.M., Weidner S., Wong K., Buhrmester J., Chain Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie Golding B., Puehler A.;
                                                                          SLR1210.
                                                                                                                                     P73361
                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                            none;
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                                                                                                                                                                                                                             Local Similarity tes 4; Conserv
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12870 MW;
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12,
19,
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                                                     Chroococcales;
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                                                              PCC 6803)
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Last sequence update)
Last annotation updat
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Pred.
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Pred. No.
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No.
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                                                     Synechocystis
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Tanaka

Α.,

Asamizu

Nakamura

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RESULT
Q9NBK3
ID Q9
AC Q9
DT 01
DT 01
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DT Rii
GN RP
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Best Local :
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Best Local
Q9NBK3

Q9NBK3;
Q9NBK3;
Q9NBK3;
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q99WV3 PRELIMINARY; PRT; 130 AA. Q99WV3; O1-JUN-2001 (TrEMBLrel. 17, Created) O1-JUN-2001 (TrEMBLrel. 17, Last sequence update) O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                    Lancet 357:1225-1240(2001).
EMBL; AP003358; BAB56435.1; -.
EMBL; AP003130; BAB41486.1; --
HYpothetical protein; Complete
SEQUENCE 130 AA; 15765 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus (strain Mu50 / ATCC Staphylococcus aureus (strain N315). Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=S.aureus (strain Mu50), an MEDLINE=21311952; PubMed=11418146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein SAV0273. SAV0273 OR SA0262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=158878,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D90905; BAA17392.1; -. Hypothetical protein; Complete SEQUENCE 129 AA; 14936 MW;
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Hosouchi T., Matsuno
Shimpo S., Takeuchi (
Tabata S.;
                                                                                                                           41
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                                                                                                                                                                              1 SYDA 4
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4; Conservative
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ilarity 100.0%;
Conservative (
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Matsuno A., Muraki A., Nakazaki N., Naruo K.
Akeuchi C., Wada T., Watanabe A., Yamada M.,
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100.0%; F
tive 0;
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Pred. No. 9.5e+02;
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); Mismatches
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A3F692D13BD7B764 CRC64;
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AD6EF19018322DEA CRC64;
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aruo K., Okumura
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Q8X858;
Q1-MAR-2002 (TrEMBLrel. 2001-MAR-2002 (TrEMBLrel. 2001-MAR-2001-MAR-2002 (TrEMBLrel. 2001-MAR-2002 (TrEMBLrel. 2001-MAR-2002 (TrEMBLrel. 2001-MAR-2002 (TrEMBLrel. 2001-MAR-2002 (TrEMBLrel. 2001-MAR-2002 (TrEMBLrel. 2001-MAR-2002 (TrEMBLrel. 2001-MAR-2001-MAR-2001-MAR-2001-MAR-2001-MAR-2001-MAR-2001-MAR-2001-MAR-2001-MAR-2001-MAR-2001-MAR-2001-MAR-2001-MAR-2001-MAR-2001-MAR-2001
                                                                                                  STRAIN=0157:H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino K., Ohnishi M., Kurokawa C., Ogasawara N., Yobe T. Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterchemorrhagic Escherichia coli Ol57:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

EMBL; ABO05257; AAG55129.1; -.

EMBL; ABO05253; BAB34258.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                              Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE-20428552; PubMed-10970881; |
Mitrovich Q.M., Anderson P.;
"Unproductively spliced ribosomal protein mRNAs
"Unproductively spliced ribosomal protein mRNAs
"Unproductively spliced ribosomal protein mRNAs
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NCBI_TaxID=83334;
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Escherichia coli O157:H7.
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Genes Dev. 14:2173-2184(2000).
-!-SIMILARITY: BELONGS TO THE LIP
EMBL; AF247848; AAF77029.1; -.
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Rhabditidae;
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e; Peloderinae;
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RESULT 43
ONUK1
ID OPXUK
AC QPXUK
DT 01-WC
DT 01-DE
DE W07G1
GN W0
RESULT 44
Q97HFB
ID 097HFB
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                                                                                                SEQUENCE FROM N.A.

STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; PubMed-11466286;

MOEDLINE-1359325; PubMed-11466286;

NOEILINE-JJ. Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing

"Genome sequence and comparative analysis of the solvent-producing

Bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838 (2001).

EMBL; ARD07699; ARX79882 1; -

InterPro; IPR000424; SSB_protein.

Pfam; PF00436; SSB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium acetobutylicum.

Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
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Science 282:2012-2018(1998).
EMBL; 282076; CAB04936.1; -.
SEQUENCE 133 AA; 15587 MW;
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01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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14980 MW;
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100.0%; Pred. No. 9.7e+02;
tive 0; Mismatches 0;
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FOFCOOCEBF938EDB CRC64;
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RESULT 45
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STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; PubMed-11466286;

MEDLINE-21359325; PubMed-11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

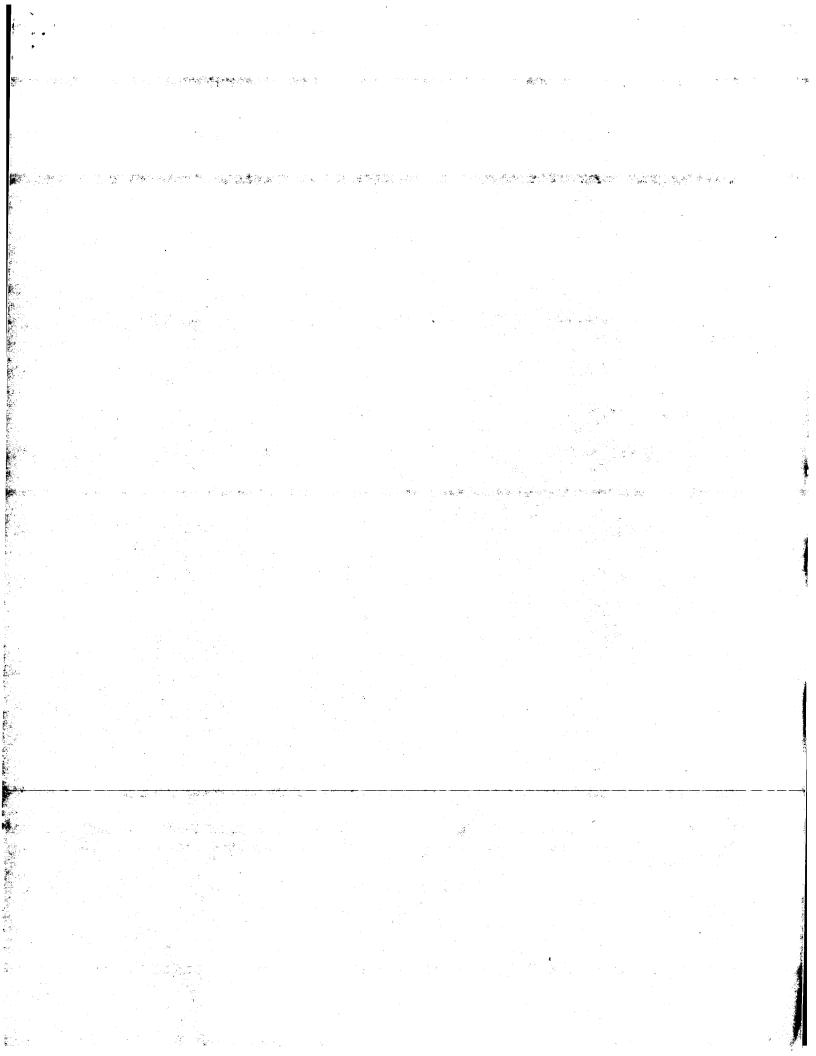
J. Bacteriol. 183,4823-4838(2001).

EMBL; AE007774; AAK80711.1;

Complete proteome.

REGIENCE 133 AA. 14776 MS. AE07DA2063381FIC CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q97FH2;
                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence up
01-OCT-2001 (TrEMBLrel. 18, Last annotation
                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                 Clostridium acetobutylicum.
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                                                   56 SYDA
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                                                                                                     Score 21; DB Pred. No. 9.7

Mismatches
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Pred. No.
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9.7e+02;
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9.7e+02;
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                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                           Score
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19.150 Million cell updates/sec
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/SIDS2/gcgdata/genesedy-genesedp-embl/AA1989.DAT:*

/SIDS2/gcgdata/genesedy-genesedp-embl/AA1999.DAT:*

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/SIDS2/gcgdata/genesedy-genesedp-embl/AA1994.DAT:*

/SIDS2/gcgdata/genesedy-genesedp-embl/AA1994.DAT:*

/SIDS2/gcgdata/genesedy-genesedp-embl/AA1995.DAT:*

/SIDS2/gcgdata/genesedy-genesedp-embl/AA1995.DAT:*

/SIDS2/gcgdata/genesedy-genesedp-embl/AA1999.DAT:*

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/SIDS2/gcgdata/genesedy-genesedp-embl/AA1999.DAT:*

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       AAR72768
AAW70154
AAW46010
AAY96208
AAY83850
AAE05612
AAW13438
AAB07398
AAX56002
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Mammalian ribonucl
peptide produced b
Peptide #1 based
Arabidopsis AHAS s
Ribonucleotide red
N-terminal CT27 pe
Brain homing pepti
Brain homing pepti
Brain homing septi
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AAW10869	AAY95418	AAW31683	AAR71050	AAW10854	AAU88904	ABB51179	AAR33356	AAY36691	AAY91397	AAR36604	AAY95420	AAR93618	AAM97480	AAM97105	AAY93098	AAY92950	AAB84497	AAG79149	AAB20756	AAW74421	AAW69624	AAY93093	AAY93009	AAY93008	AAY93007	AAY92947	AAG86956	AAW61058	AAR72570	AAB99639	AAY93097	AAU10715	ABG67883	AAE11804
MAb anti-HBsAg bin	Anti-angiogenic D3	ium perf	a.	MAb anti-HBsAg bin	Insulin/insulin-li	cret	of	Fragment of human	Human secreted pro	N-terminus of 37 k	-	rincipal	peptide	æ		Transforming growt	Amino acid sequenc	Amino acid sequenc	libr	agonist				-		Ω	omyces cer	3	111ium		forming grow	homin	ADPI trypt	Phage peptide #12

ALIGNMENTS

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RESULT 1
AAR72768
Key
Modified-site
                                                                                                                                                                            Plasmodium falciparum; mammalian; ribonucleotide reductase; R2 subunit; C-terminal region; inhibitor; antimalarial therapy; Pf RR; parasite.
                                                                                                                                                           Synthetic
       WPI; 1995-161730/21
                       Cooperman BS, Fisher AL,
                                      (UYPE-) UNIV PENNSYLVANIA.
                                                        14-OCT-1993;
                                                                        07-OCT-1994;
                                                                                          20-APR-1995.
                                                                                                           WO9510526-A1
                                                                                                                                                                                                       Mammalian ribonucleotide reductase inhibitory peptide.
                                                                                                                                                                                                                        02-FEB-1996
                                                                                                                                                                                                                                                         AAR72768 standard; Protein; 7
                                                                                                                                                                                                                         (first entry)
                                                         93US-0136743
                                                                         94WO-US11416
                                                                                                                                     Location/Qualifiers
                                                                                                                            /note= "opt. acylated"
                       Rubin H,
                        Salem
                        J,
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AAU68419

Breast cance

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RESULT 2
AAW70154
ID AAW7
XX AAW7
AC AAW7
AC AAW7
XX G1yc
KW Fast
KW Fast
KW Fast
KW Fook
OS Mycc
XX W098
XX W098
XX IN W098
XX W099-J
XX 31-L
XX W1-L
XX WPI
PR S1-L
XX WPI
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s AAW70114, AAW70142-W70154 are N-terminal amino acid sequences dees generated by chymotrypsin/trypsin digestion of the 45 kDa Mpp protein. These sequences were obtained by purifying the 45 kDa digesting it with chymotrypsin/trypsin, and then separating the by reversed-phase HPLC on a column. All of the peptides were
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                                                                                                                                                                             Peptides AAW45983-W456025 are based on portions of somatostatin, somatostatin receptors (SSTR) and insulin-like growth factor binding proteins (IGFBP). They are capable of increasing weight gain, birth weight, growth rates, milk production, levels of circulating insulin, IGF-I and IGF-III, fibre production and muscle weight. They may be used to modulate carbohydrate metabolism and in treatment of diabetes. The oil carrier may be used for delivery of the peptides.
                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 9;
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                                                                                                                                                                                                                                                                                                                                                                   136pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DJ,
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                                                                               .0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Westbrook SL;
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                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                               Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                           DB 19;
7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .8e+05;
                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           somatostatin;
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                            growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                 on portions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        further work
                                                      0;
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                                                      Gaps
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                                                                                                                                                                               Arabidopsis acetohydroxy-acid synthase (AHAS) small subunit is needed CC for branched-chain amino acid synthesis and so is essential for life. CC AHAS is also known as acetolactate synthase. Inhibition of this enzyme CC in plants would lead to plant death and therefore inhibitors would be potential herbicides. Certain herbicides are known to inhibit AHASs: CC imidazolinones, sulfonylureas, triazolpyrimidine sulfonamides. CC pyrimidyl-cvy-benzoic acids, sulfamoylureas and sulfonylureatoxamides. CC Mutant AHAS may be resistant to these herbicides and may be used to CC create herbicide resistant transgenic plants e.g. dicot and monocot crop CC plants. A thrombin cleavage site was incorporated into an AHAS small companies. A thrombin cleavage site was incorporated into an AHAS small companies. A thrombin cleavage site was incorporated into an AHAS small companies. The glutathione CC transferase was then cleaved via the thrombin cleavage site. Cleavage transferase was then cleaved via the thrombin cleavage site. Cleavage companies, in that the glycine and serine residues of the cleavage site CC are maintained on the AHAS protein. The present sequence details the CC are maintained on the AHAS protein. The present sequence details the CC are maintained on the AHAS protein and serine residues of the cleavage site CC are maintained on the AHAS protein. The present sequence details the CC and filarion due to cleavage.
                                                                   Matches
                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide encoding eukaryotic acetohydroxy-acid synthetase small subunit protein for producing transgenic herbicide resistant protein for producing transgenic herbicide resistant small identifying mutations affecting enzymatic activity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acetolactate synthase; imidazolinone; sulfonylurea;
triazolopyrimidine sulfonamide; sulfamoylurea; enzyme;
triazolopyrimidyl-oxy-benzolc acid; sulfonylcarboxamide; transgenic plant;
                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kakefuda G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96208 standard; Peptide;
                                                                                                                                                                        modification due
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMCY ) AMERICAN CYANAMID CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               branched-chain
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                                                                                   Local Similarity
N
                                1 SLDA 4
SLDA
                                                                   4.
                                                                                                                                      7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AHAS small subunit F2 gene fragment N-terminal sequence
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Costello C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                        cleavage.
                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acetohydroxy-acid synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 AA.
                                                                   0;
                                                               Score 18; DB Z1;
Pred. No. 7.8e+05;
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                                                                                                 Length
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                                                                   Indels
                                                                 0;
                                                                 Gaps
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RESULT 5

Mycobacterial disease; infection; 88-kDa protein; tuberculosis; human immunodeficiency virus; HIV; CT27 glycopeptide; serodiagno

peptide obtained by proteolysis of Mt 45 kDa antigen

0

N-terminal CT27

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RESULT 6
AAE05612
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ID AAY8
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                                                                                                                                                                    δÃ
                                                                                                                                                                                          Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                      The invention relates to a composition comprising a peptide inhibitor of ribonucleotide reductase. Peptides AAY83838-Y83864 represent examples of the inhibitor peptides used in the composition. The peptides are synthesised based on the sequences of known mammalian, bacterial and viral ribonucleotide reductases. The compositions are used in the treatment of disorders associated with DNA replication, such as tumour growth and metastasis and infectious disease, such as those caused by viruses, bacteria, fungi and parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; antibacterial; virucide; antifungal; parasiticide; virus; antimetastatic; ribonucleotide reductase; peptide inhibitor; bacteriu DNA replication; tumour growth; metastasis; fungus; parasite.
                                                                                                                                                                                                                                                                                                                                                                          AAY83850;
                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribonucleotide reductase inhibitor peptide #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY83850 standard; peptide;
                                                                         AAE05612;
                                                                                            AAE05612 standard; peptide; 7
                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Barwis
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cooperman BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-AUG-1996;
28-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYPE-) UNIV PENNSYLVANIA
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                                                                                                                                                               1 SLDA 4
                                                                                                                                                   SLDA
                                                                                                                                                                                                                                                                                                                                                                                                                     2000-223191/19
                                                                                                                                                                                           4;
                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                      Column 4;
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         Nair S, Fisher A,
                                                                                                                                                                                                                                     AA;
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                                                   (first entry)
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97US-0919748.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "acetylated N-terminus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                     92pp; English.
                                                                                                                                                                                           0;
                                                                                                                                                                                                    Score 18; DB 21;
Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Laub P, S
Smith AB;
                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasho
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                                                                                                                                                                                                              Length
                                                                                                                                                                                           Indels
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                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacterium;
                                                                                                                                                                                           Gaps
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RESULT 7
AAW13438
ID AAW1
XX
AC AAW1
XX
DT 15-J
XX
Brai
XX
Brai
XX
Brai
XX
Brai
XX
Synt
XX
PN W097
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                                                                                                                                                                                                                                                                                                                      γ
                                                                                                                                                                                                                                                                                                                                                                                                                             CC mycobacterial disease or infection comprises assaying a biological fluid CC sample for the presence of early antibodies specific for an 88 kpa CC Mycobacterium tuberculosis (Mt) protein or immune complexes consisting of CC an 88 - kpa M tuberculosis protein antigen or immune complexes consisting of CC specific for the antigen. The method is useful for the antibody CC detection of mycobacterial disease, particularly tuberculosis, in CC individuals at heightened risk of developing tuberculosis (TB). This CC individuals include human immunodeficiency virus (HIV)-infected subjects or other immunocompromised individuals. The method is a rapid and CC inexpensive screening procedure for detecting mycobacterial disease. CC The present sequence is the N-terminal amino acid sequence of CT27 CC glycopeptide. The N-terminal appetide is identified by fast atom CC sequence analysis of peptides generated by proteolysis of the Mt 45 kba/MPT 32 glycoprotein with chymotrypsin/trypsin. The Mt 45 kba/MPT 32 early antigen is used in the serodiagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
              W09710507-A1
                                                                        Brain homing peptide; in vivo panning; screening; phage display;
                                                                                                                  Brain homing
                                           Synthetic
                                                                                                                                                                                   AAW13438;
                                                                                                                                                                                                           AAW13438 standard; Peptide; 8
                                                                                                                                                  15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Column 46; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen-antibody complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting a mycobacterial disease (tuberculosis) in individuals comprise assaying a biological sample for the presence of anti-Mycobacterium tuberculosis antibodies or M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laal S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fast atom bombardment-mass spectrometry; FAB-MS; proteolysis,
45 kDa glycoprotein; MPT 32; chymotrypsin; trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYNY-) UNIV NEW YORK MEDICAL (COLS ) UNIV COLORADO STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JAN-1997;
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                                                                                                                                                                                                                                                                                                                         1 SLDA 4
                                                                       delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention relates to a method for early detection of active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-424324/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zolla-Pazner
                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                  peptide
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                AA;
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                                                                                                                                                                                                                                                                                                                                               100.0%; s
100.0%; f
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Belisle
                                                                                                                                                                                                                                                                                                                                            Score 18; DB 22;
Pred. No. 7.8e+05;
Mismatches 0;
                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CENT.
                                                                                                                                                                                                                                                                                                                                                                         Length 7;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                            0;
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RESULT 8
AAB07398
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Best Local :
                                11-SEP-1995;
10-MAR-1997;
       (BURN-) BURNHAM INST
                                                                    23-JUN-1997;
                                                                                                                   US6068829-A
                                                                                                                                                                                        Mus sp
                                                                                                                                                                                                         Brain; homing peptide; organ targeting; tissue targeting; mouse; cyclic
                                                                                                                                                                                                                                       Brain homing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This synthetic peptide is an example of a brain-homing peptide that was identified using a claimed method for obtaining molecules that home to a selected organ or tissue. This in vivo panning method typically involves administering a phage display library to a subject, and identifying expressed peptides which home to the desired organ or tissue. The isolated peptides which vascular tissue or tumour tissue. The isolated peptides (see AAW13412-52, AAW1181-86) can be used to target e.g. drugs, toxins o labels to the selected organ/tissue (claimed) or to identify and/or isolate target molecules (claimed): The peptides can be directly methods, which require further examination to see if they maintain specificity in vivo.
                                                                                                                                                      Disulfide-bond
                                                                                                                                                                                                                                                               17-OCT-2000
                                                                                                                                                                                                                                                                                       AAB07398
                                                                                                                                                                                                                                                                                                           AAB07398 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Obtaining compound that homes to selected organ or tissue - by vivo panning method, specifically to identify brain, kidney, angiogenic vasculature or tumour tissue homing peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-202359/18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LJOL-) LA JOLLA CANCER RES FOUND.
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11-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 18; DB 18; llarity 100.0%; Pred. No. 7.8e+05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                      peptide # 12.
                                                                                                                                                                                                                                                            (first entry)
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                              95US-0526710.
97US-0813273.
                                                                   97us-0862855
                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruoslahti E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0526710
95US-0526708
                                                                                                                                         /note=
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                                                                                                                                       "Can optionally form a
                                                                                                                                                                                                                                                                                                           æ
                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                      cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                    peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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RESULT 9
AAY56002
ID AAY5
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence to identified by using in vivo panning to screen a library organ homing molecules. The present sequence can be used moiety to a the brain tissue, by linking the moiety to the moiety are of potential moieties are drugs, toxing the moiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying and recovering organ homing molecules or peptides by in vivo panning comprises administering a library of diverse peptides linked to a tag which facilitates recovery of these peptides -
                 sequence for isolating the corresponding gene. The protein is useful for the specific cleavage of complex sugar chains for the preparation, investigation and modification of these chains, especially in complex carbohydrates forming part of a glycoprotein molecule which undergoes
                                                                 Peptides AAY55994-Y56014 represent fragments of the Mucor hiemalis endo-beta-N-acety/glucosaminidase protein derived by cleavage with Lys-C protease and subsequent amino acid sequencing. The peptide sequences were then used to generate primers to isolate the coding
                                                                                                                                                   Polynucleotides encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example
                                                                                                                               Example 4;
                                                                                                                                                                                         WPI; 2000-062704/05
                                                                                                                                                                                                                 Kobayashi K,
Yoshida S;
                                                                                                                                                                                                                                                                             22-MAY-1998;
                                                                                                                                                                                                                                                                                                     20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                     WO9961591-A1
                                                                                                                                                                                                                                                                                                                                                                           Mucor hiemalis.
                                                                                                                                                                                                                                                                                                                                                                                                  Endo-beta-N-acetylglucosaminidase; enzyme; cleavage; sugar chain;
carbohydrate; glycoprotein; disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mucor hiemalis endo-beta-N-acetylglucosaminidase peptide p60-AP-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY56002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY56002 standard; peptide; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detectable label.
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                                                                                                                                                                                                                                                     (KIRI ) KIRIN
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                                                                                                                              Page 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Column 17; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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          'n
                                                                                                                                                                                                                                                     BEER KK.
                                                                                                                                                                                                                              Takeuchi
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                                                                                                                              72pp; Japanese
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        such
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Pred. No.
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. 7.8e+05;
ches 0;
                                                                                                                                                                                                                             Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide. This sequence ver a library of potential can be used to direct a
                                                                                                                                                                                                                           ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 8;
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                                                                                                                                                                                                                             Kumagai
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RESULT 10
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         Query Match
Best Local Similarity
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                                                                                                                                                                           or identifying the risk of a subject developing cancer (especially breast cancer), or monitoring the effect of therapy on a subject with cancer, comprising analysing a test sample using two-dimensional electrophoresis and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The methods disclosed are used for the diagnosis and prognosis of breast cancer, for determining the severity of breast cancer, and for identifying a subject at risk of developing breast cancer, and monitoring the effect of therapy administered to a subject. Antibodies raised against the binding domain of a BPI, the binding domain of a BPI, a nucleic acid encoding a BPI, or a nucleic acid that inhibits the function of a BPI can be incorporated into a pharmaceutical
                                                                                                   composition for treating or preventing breast cancer. The methods use sensitive and specific biomarkers provide early diagnosis of breast cancer, and the compositions are more potent, specific, and has a more rapid effect with fewer side effects that other prior art methods. The present sequence is a tryptic digest peptide from a BPI of the
                                                                                                                                                                                                                                                                                                                                                     The
                                                                                                                                                                                                                                                                                                                                                                                                               Identifying proteins for clinical screening, diagnosis and preast cancer, comprises detecting Breast Cancer-Associated Isoforms (BPIs) using two-dimensional electrophoresis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Breast cancer-associated protein isoform; br immunogen; cytostatic; BPI; tryptic digest peptide.
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                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 51; 197pp; English
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24-MAR-2000; 2000GB-0007265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Breast cancer-associated protein isoform, BPI-247 peptide #3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herath HMAC,
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                                                                                                                                                                                                                                                                                                                                                   invention relates to diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Peptide;
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llarity 100.0%;
Conservative (
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              100.0%;
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O; Mismatches
Score 18; DB 22;
Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parekh RB,
                                                                                                                                                                                                                                                                                                                                                   determining the stage or severity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.8e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterfield MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      breast cancer;
                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 8;
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1 SLDA 4

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Conservative

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Indels

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Gaps

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RESULT 11
AAE11804
ID AAE11
XX AAE11
XX AAE11
XX AAE11
XX AAE11
XX AAE11
AC AAE11
AC AAE11
AC Phage
XX Enric
CX Bacte
YX Local
XX Fall
XX Enric
YX 
RESULT 12
ABG67883
ID ABG67
XX
AC ABG67
XX
DT 07-OC
XX
DE Human
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           Human ADPI tryptic digest peptide #592.
                                                                               07-OCT-2002
                                                                                                                                                                                    ABG67883 standard;
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11-SEP-1995;
10-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an enriched library fraction containing molecules that selectively home to a selected organ or tissue such as brain, kidney or tumour recovered by in vivo panning. The invention generally relates to the field of molecular medicine, drug delivery and to a method of invivo panning for identifying a molecule that homes to a specific organ. The molecules, e.g., peptides, peptidenmetics, proteins and fragments of proteins contained in an enriched library fraction may be administered to a subject as part of a pharmaceutical composition to rest disease or in diagnostic methods. The present sequence is a peptide from bacteriophage targetted to brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enriched library fraction comprising molecules recovered by in vivo panning that selectively home to a selected organ or tissue useful for treating disease or in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Column 17; 21pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6296832-B1
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                                                                         (first entry)
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95US-0526710.
97US-0813273.
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                                                                                                                                                                                    Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 22;
Pred. No. 7.8e+05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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RESULT 13
AAU10715
ID AAU10
XX AAU10
AC AAU10
XX 12-MA
CT 12-MA
XX U2-MA
XX Organ
KW Organ
KW deliv
XX
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                                                                                                                                                                                                                                                        QΥ
                                                                                                                                                                                                                                                                                                                                                               The present invention relates to methods and compositions for the CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in CC a subject. The method comprises analysing a sample of brain tissue from a subject by 2D electrophoresis to generate a 2D array of.
CC Alzheimer's disease-associated features (ADFS), whose relative CC abundance correlates with the presence, absence, stage or severity of CC that chosen feature in brain tissue from persons free from AD. The CC invention also describes Alzheimer's disease-associated protein CC invention also describes Alzheimer's disease-associated protein CC compositions of the invention are useful for the screening, diagnosis CC or prognosis of AD in a subject, for identifying's subject at risk of developing AD, CC or for monitoring the effect of therapy administered to a subject having AD. Antibodies capable of binding to ADPIS are useful for treatment regime. An agent that modulates the activity of ADPI is cuseful in the manufacture of a medicament for the treatment or CC prevention of AD in a subject. ABG67292-ABG68038 represent human ADPI ax
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                        12-MAR-2002
                                                                                                                                            AAU10715 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening, diagnosis or prognosis of Alzheimer's disease in subject, comprises detecting Alzheimer's disease-associated features or Alzheimer's disease-associated protein isoforms in brain tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI; Alzheimer's disease-associated feature; neuroprotective; Alzheimer's disease-associated protein isoform; nootropic; ADPI tryptic digest peptide.
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                                                                                                                                                                                                                             \vdash
                                                                                                                                                                                                                             SLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the subject
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                                                                                                                                                                                                                             4
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                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                 ÃĀ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parekh
                                                                                     entry)
                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RВ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rohlff C;
                                                                                                                                                æ
                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                Score 118;
Pred. No.
                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                7.8e+05;
thes 0;
                                                                                                                                                                                                                                                                                                              DB 23;
                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                              œ
                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                Gaps
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Organ targeting; tissue targeting; cancer; tumour homing molecule

brain

homing

Brain homing peptide #12 useful for delivery of target molecules.

0

delivery of target molecule;

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RESULT 14
AAY937
ID 9AY93
XX AAY93
XX AAY93
XX O8-NC
DT 08-NC
DT 17ans
XX Hepat
KW Hepat
KW Compp
KW extra
XX
XX Homo
XX Homo
XX Homo
XX Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                         ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comparison and the present at the method comparison administering to the subject the library of diverse molecules, collecting a sample of the selected organ or tissue (e.g. brain or kidney), and recovering from the seample several molecules that home to the selected organ or tissue (c.g. brain or kidney), and recovering from the sample several molecules that home to the selected organ or tissue. CC The method is useful for identifying molecules, particularly useful for cs screening large number of molecules (e.g. peptides), that home to a specific organ. The identified molecule is useful for e.g. raising an CC e.g. drug, toxin or detectable label) to the selected organ. CC specifically, the method is useful for identifying a desired molecule organ to a subject by linking an appropriate moiety to a tumour homing consciule. The present method provides a direct means for identifying CC molecules that specifically home to a selected organ and, therefore provides a significant advantage over previous methods, which require that a molecule identified using an in vitro screening method considered to examined to determine if it maintains its specificity in the present method provides a direct mointains its specificity in the present method to determine if it maintains its specificity in the present method is useful for the selected organ and, therefore that a molecule identified using an in vitro screening method to determine if it maintains its specificity in the present method provides a significant advantage over previous methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUN-1997;
11-SEP-1995;
10-MAR-1997;
                                                                         Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; lextracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                     Transforming growth factor inhibitory peptide P143.
                                                                                                                                                                                                08-NOV-2000
                                                                                                                                                                                                                                                                          AAY93097 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Column 17; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recovering molecules that home to an organ or tissue, useful for identifying molecules that home to a specific organ or tissue, e
WO200031135-A1
                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruoslahti E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6306365-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identifying a tumour homing molecule by in vivo panning of a library -
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity es 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                             1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to a method of recovering molecules that
                                                                                                                                                                                                                                                                                                                                                                        IIIII
SLDA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                            (first entry)
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95US-0526710.
97US-0813273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0227906.
                                                                                                                                                                                                                                                                        peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; S
100.0%; P
ative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;
                                                                                                                                                                                                                                                                          9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 23;
Pred. No. 7.8e+05;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to identify the presence of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                liver
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15-DEC-1999; 14-DEC-2000;

99EP-0125035.

2000WO-IL00833

21-JUN-2001 WO200143691-A2 Homo sapiens Synthetic.

gastritis; ulcer;

thrombosis;

allergy;

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RESULT 15
AAB99639
В
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-b1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis.
                                                                                                                                                                            rheumatoid arthritis; myasthenia gravis; systemic lupus erythematosis; chronic inflammation; atherosclerosis; inflammatory bowel disease; reactive arthritis; chronic infection; graft rejection; gingivitis;
                                                                                                                                                                                                                       pro-inflammatory immune response; immune system; inflammatory disease immunostimulatory; antilifammatory; antidiabetic; immunosuppressive; antitheumatic; nootropie; antiarteriosclerotic; antimicrobial; antiul neuroprotective; autoimmune disease; diabetes; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                  Human hsp60
                                                                                                                                                                                                                                                                                                                                                                                                           AAB99639 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides that antagonize binding of transforming growth factor betal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ezquerro Saenz
Borras Cuesta F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUN-2000
                                                                                                                                                                                                                                                                                                                                                04-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-411935/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-NOV-1999; ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SLDA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SLDA 4
                                                                                                                                                                                                                                                                                    heat shock protein; hsp60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for treatment of liver disease, l sequences of the factor or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page
                                                                                                                                                                                                                                                                                                                 derived peptide #65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.
                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98ES-0002465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-ES00375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; 86pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lasarte Sagastibelza JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                 inhibition; antagonist; antiallergic;
immune system; inflammatory disease;
                                                                                                                                                               graft rejection; gingivitis; acute infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      especially cirrhosis, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 7.8e+05; thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enzymes able to degrade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                        antiulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 16
AAA772570
ID AAA772
XX AAA772
XX Penic
DT 23-NO
DE Penic
KW Penic
KW inulo
OS Penic
XX Penic
XX Penic
YX 17070
AX 17070
AX 23-AU
XX 23-AU
XX WPI;
XX WPI;
XX WPI;
XX PT A new
PT A new
PX inulc
XX Disc:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
Disclosure; Page 7; 8pp; Japanese
                                   A new DNA encoding endo-inulinase - inulo-oligosaccharides
                                                                                                                                                   23-AUG-1993;
                                                                                                                 (MITK ) MITSUI TOATSU CHEM INC
                                                                                                                                                                                                                                                   JP07059574-A
                                                                                                                                                                                                                                                                            Penicillium purpurogenum
                                                                                                                                                                                                                                                                                                      Penicillium purpurogenum variety rubrisclerotium; endo-inulinase; inulo-oligosaccharides; inulin; peptide fragment 175-184.
                                                                                                                                                                                                                                                                                                                                                    Penicillium purpurogenum endo-inulinase peptide fragment 175-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR72570 standard; Peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunosuppressive, notropic, antiarteriosclerotic, antinicrobial, antilulcer, antiallergic and neuroprotective activities. The antagonists are useful in the treatment of an inflammatory disease or disorder, e.g. an autoimmune disease, diabetes, multiple sclerosis, rheumatoid arthritis, myasthenia gravis, systemic lupus erythematosis, chronic inflammation, atherosclerosis, inflammatory bowel disease, reactive arthritis, chronic infections, graft rejection, gingivitis, gastritis, ulcer, thrombosis, allergy and acute infections. AAH43896 to AAH43899 and AAB99542 to AAB99673 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes anti-inflammatory peptides of heat shock protein hsp60, which are capable of acting as antagonists of hsp60 characterised by their ability to reduce or prevent the induction of a pro-inflammatory immune response of cells of the innate immune system by hsp60. The peptides have antiinflammatory, antidiabetic, antirheumatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-inflammatory peptides of hsp60, which are capable of acting as antagonists of hsp60, useful for treating an inflammatory disease or disorder, e.g. an autoimmune disease, diabetes, multiple sclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kolb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 9; Page 58; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-390150/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                  93JP-0229448.
                                                                                                                                                                                93JP-0229448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0172297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 22;
Pred. No. 7.8e+05;
                                                 useful
                                          for the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                            of.
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RESULT 17
AAW61058
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                                         AAW61058-60 represent partial aminolacid sequence of different immunoglobulin (Ig) molecules. The specification describes a non-naturally occurring IgG having an altered amino acid sequence compared to native IgG, which binds to FCRN with increased or decreased affinity. FCRN is a receptor found on the intestinal surface of the meonate and is responsible passage of maternal milk IgG from the intestinal lumen to the systemic circulation via the intestinal epithelial cells. FCRN is also used to prevent clearance of circulating IgG from the circulation. Altering the binding site on an IgG for FCRN allows greater or lower affinity for the FCRN receptor, which subsequently increases or decreases the half-life of circulating IgG, respectively. IgG's with an increased half-life can be used to treat immune conditions or diseases such as idiopathic thrombocytopaenic
 Sequence
                           dermatomyositis.
                                                                                                                                                                                                                                                                   New antibody having altered Fc receptor binding site -
increased or decreased half-lives and clearance rates,
e.g. tumour imaging or treatment of AIDS
                                                                                                                                                                                                                                            Disclosure; Fig 2B;
                                                                                                                                                                                                                                                                                                                                                         Israel EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JUN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09823289-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                   (UYBR-) UNIV BRANDEIS.
                                                                                                                                                                                                                                                                                                                                                                                                (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawasaki disease; AIDS; Guillain-Barre syndrome; dermatomyositis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW61058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW61058 standard; peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR72567-R72575 are peptide fragments of AAR72566, the Penicillium purpurogenum variety rubrisclerotium endo-inulinase. The endo-inul can be used to prepare an inulo-oligosaccharide from inulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity es 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 SLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SLDA 4
                                        (ITP),
 10
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                                                                                                                                                                                                                                                                                                                                                         Simister
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          idiopathic thrombocytopaenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IgY used in the course
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                     Kawasaki disease,
                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0031607
                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US21437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IgG;
                                                                                                                                                                                                                                           32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FcRn binding; half-life;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred:
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                                     AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                  Guillain-Barre syndrome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16;
1.5e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          purpura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     increase; decrease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                  for,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Query Match Best Local Similarity

100.0%;

Score 18; Pred. No.

DB 19; 1.5e+02;

Length

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RESULT 19
AAY92947
ID AAY92
XX
AC AAY92
XY
OB-NC
XX
DE Trans
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KW Hepat
KW compe
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AAG86956
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                       The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from
Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver;
                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200142276-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG86956 standard; Peptide; 10 AA
                                                             08-NOV-2000
                                                                                     AAY92947;
                                                                                                          AAY92947 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying complementary peptides by nucleotide sequence databases, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-367863/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae;
drug discovery; drug desi
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                                   Transforming growth factor inhibitory peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PROT-) PROTEOM LTD
                                                                                                                                                                                                                     Local Similarity
nes 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                       English.
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                                                                                                                                                                                                                     Score 18; DB 22;
Pred. No. 1.5e+02;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                              analysis of protein in drug design -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1905
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                                                                                                                                                                                                                                           Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY93945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease. specifically cirrhosis
                                                                                                                                                                                                                                                                          Rattus sp.
                                                                                                                                                                                                                                                                                                                               Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 80; 86pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      partial sequences of the factor or its receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200031135-A1
                                                 24-NOV-1998;
                                                                                                      23-NOV-1999;
                                                                                                                                                                                                                     WO200031135-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                              Transforming growth factor inhibitory peptide P53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY93007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY93007 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-411935/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         liver disease, specifically cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CIEN-)
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les 4; Conserv
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Pred. No.
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ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth factor betal,
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(CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.

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Best Local
                   Disclosure; Page 27; 86pp; Spanish.
                                            Peptides that antagonize binding of transforming useful for treatment of liver disease, especially partial sequences of the factor or its receptors
                                                                                                                             Ezquerro Saenz
Borras Cuesta I
                                                                                                                                                                                                                                                                                                                         Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; lextracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of
                                                                                                                                                                     (CIEN-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ezquerro Saenz IJ,
Borras Cuesta F;
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                                                                                                                                                                 INST CIENTIFICO & TECNOLOGICO NAVARRA
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Conservative (
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); Mismatches
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                                                                                                                                                                                                                                                                                                                        mimetope; cirrhosis
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                                                        growth factor beta1,
y cirrhosis, are
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invention relates to

synthetic

peptides that antagonise

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RESULT 22
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                      The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-b1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis.
                                                                                                                                                                       The invention relates to of transforming growth
                                                                                                                                                                                                                       Disclosure; Page 27; 86pp; Spanish.
                                                                                                                                                                                                                                                  Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors -
                                                                                                                                                                                                                                                                                                                                                         Ezquerro Saenz IJ,
Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatotropic; antagonist; transforming growth factor betal; TGF-b1; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                       24-NOV-1998;
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RESULT 23
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Best Local Similarity
                                                                                                                                                                                                                                           The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides ANY22945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; l extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors -
            AAW69624 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 31; 86pp; Spanish
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Borras Cuesta F;
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Pred. No. 1.9e+02;
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Pred. No. 1.9e+02;
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RESULT 25
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Best Local
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20-SEP-1994;
13-OCT-1994;
                                                                                                                                                                                                                                                                                                     a function naturally performed by the corresponding yeast pheromone system protein; and (b) a second heterologous gene encoding a heterologous peptide, where the heterologous peptide modulates the interaction of the surrogate with the pheromone system in the yeast cell, and the modulation is a selectable or screenable event. The yeast cells are used in assaying a peptide for modulation of the activity of a non-yeast surrogate for a pheromone system protein and determining by detecting a change in the selectable or screenable event whether the pheromone signal pathway is activated or inhibited by the interaction of
                                                                                                                                                                                                                                                                 of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a yeast cell having a pheromone system, in which the cell comprises: (a) a first heterologous gene encoding a heterologous surrogate of a yeast pheromone system protein, the surrogate being a kinase and performing in the pheromone system of the yeast cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant yeast cells - con system protein surrogate and
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N-PSDB; AAV40413.
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31-MAR-1993;
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                                                              AAW74421 standard;
                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                             pheromone signal pathway is activated or inhibited by the interaction the surrogate and the peptide. The present sequence represents an Ste2 agonist from the alpha-Mid-5 library which is from an example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Column 143; 93pp; English.
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93US-0041431.
94US-0190328.
94US-0309313.
94US-0322137.
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                                                              peptide;
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and gene encoding peptide
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                                                                                                                                                                                               Score 18;
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AAW74421;

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10-MAY-1999

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31-JAN-1994;
20-SEP-1994;
13-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents an Ste2 agonist peptide sequence. The invention relates to yeast cells engineered to express an exogenous protein capable of substituting for a yeast protein involved in the post-translational modification, transport, recognition or signal transduction of a yeast pheromone. The system can be used to identify drugs which inhibit or activate the ability of the surrogate to substitute for the cognate yeast pheromone system protein. Inhibitors of farnesyl transferase identified can be used for anticancer therapies.
US6100042-A
                                             Saccharomyces Synthetic.
                                                                                                                                         Yeast; pheromone; alpha-factor; transporter; pheromone receptor; G alpha subunit; MF alpha 1; MFal; STE2; STE3; C5a receptor; GPA G protein coupled receptor; mutagenesis; amplification; screeninhybrid; agonist; antagonist; signal transduction; detection;
                                                                                                                                                                                                                                                                      Alpha-Mid-5 library
                                                                                                                                                                                                                                                                                                                      21-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                       AAB20756 standard;
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DB; AAX18211.
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94US-0309313.
94US-0322137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0461598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide;
                                                                                                                                                                                                                                                                   Ste2 agonist peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agonist; cognate yeast pheromone system protein anticancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein
                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ú
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murphy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pheromone system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 13;
                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                      IJ
                                                                                                                                                                screening;
                                                                                                                                                                                                                                                                      NO:96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 27 AAG79149

AAG79149 standard;

peptide;

13

g δÃ

1 SLDA 4 | | | | | | 5 SLDA 8

0;

Amino acid 03-JAN-2002

sequence

of

an alpha-factor pheromone

(first

entry)

Cellular receptor;

ion channel; cellular activity; drug discovery;

alpha-factor pheromone

receptor ligand;

US2001026926-A1 Synthetic

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The present invention describes recombinant yeast cell mixtures (I). CC Each (I) has a heterologous G protein coupled receptor (GPCR) expressed cc in the cell membrane such that signal transduction (ST) activity via CFCR is modulated by interaction of extracellular region (ER) of GPCR with a heterologous polypeptide (P) which interacts with ER of receptor. CC Modulation of the ST activity by (P) provides a detectable signal. CC Also described is a recombinant yeast cell (II) that has a cell membrane CC which comprises a GPCR such that ST activity via GPCR is modulated by CC interaction of an ER of GPCR with an extracellular signal, and a (P) which is transported to a location allowing interaction with ER of GPCR. CC (I) is used for identifying a modulator of (P) expressed by the yeast cell which involves providing (I) which comprises heterologous GPCR and CC a heterologous test polypeptide, allowing the cells within the mixture to generate a detectable signal and then identifying the heterologous cest peptide as a modulator of the heterologous receptor protein CC expressed by the yeast cell. The yeast cells may be used to identify of the surrogate to substitute for the cognate yeast pheromone system CC the surrogate to substitute for the cognate yeast pheromone system contains. The yeast cell is also used to screen agonists and antended to screen agonists and seventhic that the exemplification of the protein surrogate to substitute for the cognate yeast pheromone system contains. The present sequence is used in the exemplification of
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1993;
31-JAN-1994;
20-SEP-1994;
                                                                                                          antagonists. The prese
the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mixture of recombinant yeast cells comprising a heterologous G populated receptor whose signal transduction activity is modulated transduction activity is modulated on the colorogous polypeptide which provides a detectable signal on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fowlkes DM,
Manfredi J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CADU-) CADUS
Local Similarity nes 4; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-531665/48
                                                                           13
100.
nilarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Broach
                                                                           A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-0041431.
94US-0190328.
94US-0309313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0322137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein
               .0%;
0
                   Score 18;
Pred. No.
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murphy AJ,
                     2e+02;
                                     DB 21;
0
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                                   Length 13;
 Indels
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0;
 Gaps
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RESULT 28
AAB84497
ID AAB84
XX AAB84
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes an assay for screening and identifying pharmaceutically effective compounds that specifically interact with and modulate the activity of a cellular receptor or ion channel. The assay uses a mixture of recombinant cells, each comprising a receptor protein whose signal transduction activity is modulated by an interaction with an extracellular signal, a recombinant gene encoding a potential receptor polypeptide, and a reporter gene construct. The assay is useful for rapid screening of large numbers of polypeptides to identify polypeptides antagonizing or agonizing receptor activity, and to identify drugs for modulating cellular activity. It is especially useful to identify ligands for orphan receptors, especially ligands for orphan cell surface receptors, which are useful in drug discovery. The present sequence represents an alpha-factor pheromone agonist, which was identified using the assay of the invention.
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05-JUN-1995;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-1996;
31-MAR-1993;
31-JAN-1994;
  03-JUL-2001
                                                                                                                                                       surrogate ligand;
                                                                                                                                                                                                                               Amino acid
                                                                                                                                                                                                                                                                                 05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 31; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identification of compounds modulating cellular receptor activity useful for identifying and screening for ligands for orphan receptors comprises using recombinant cells comprising both receptors and test polypeptide .
                                                     US6255059-B1
                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                      AAB84497 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trueheart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1995;
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13-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-DEC-2000;
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                                                                                                                                                                            protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLDA
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DB; AAI65730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                         sequence of a Ste2 agonist from alpha-Mid-5 library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murphy AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0747774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0322137.
95US-0461383.
95US-0461598.
95US-0463181.
95US-0464531.
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93US-0041431.
94US-0190328.
94US-0309313.
                                                                                                                                               receptor; GPCR; cellular receptor;
orphan receptor; Ste2 agonist.
                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 22
Pred. No. 2e+02;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Broach J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                            ion channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 29
AAY92950
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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31-JAN-1994;
20-SEP-1994;
13-OCT-1994;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The specification describes a method for identifying a ligand for an orphan G protein coupled receptor (GPCR). The method comprises rapidly screening large numbers of polypeptides in a yeast expression library to identify those polypeptides which induce or antagonise receptor bioactivity. The method is useful for screening and identifying pharmaceutically effective compounds that specifically interact with and modulate the activity of a cellular receptor or ion channel. The assay is particularly amenable for identifying surrogate ligands for orphan receptors. The present sequence represents a Ste2 agonist, identified from an alpha-Mid-5 library, using the method of the
Ezquerro Saenz IJ,
Borras Cuesta F;
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                              Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; l
                                                                                                                                                                                                                                  Transforming growth factor inhibitory peptide
                                                                                                                                                                                                                                                            08-NOV-2000
                                                                                                                                                                                                                                                                                                           AAY92950 standard; peptide; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a ligand for an orphan {\tt G} protein coupled receptor comprises using an recombinant yeast expression library -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-1996;
                                                            24-NOV-1998;
                                                                                   23-NOV-1999;
                                                                                                            02-JUN-2000.
                                                                                                                                   WO200031135-A1
                                                                                                                                                                                    extracellular
                                                                                                                                                                                                                                                                                     AAY92950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Column 57-58; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trueheart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klein
                                    (CIEN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CADU-) CADUS PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                       5 SLDA 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA,
                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                    INST CIENTIFICO & TECNOLOGICO NAVARRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
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                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                   nhibition; collagen synthesis stimulation
matrix degradation inhibitor; mimetope; c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0041431.
94US-0190328.
94US-0309313.
94US-0322137.
95US-0463181.
                                                           98ES-0002465
                                                                                  99WO-ES00375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0582333
           Lasarte Sagastibelza JJ,
                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fowlkes DM,
                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Broach J,
                                                                                                                                                                                                                                                                                                                                                                                                                                     2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                    #6
                                                                                                                                                                                                                                                                                                                                                                                                                           0
           Prieto Valtuena
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 13
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                    cirrhosis
                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paul J;
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                liver;
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RESULT 30
AAX93098
ID AAX93
AC AAX93
AC AAX92
XX Tran
XX Hepr
XW Comm
KW Hepr
XW Comm
KW ext
XX Hor
DB U2
XX Hor
AX Hor
AX Hor
XX Hor
AX Hor
A
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides ARY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the nentides are word for the collagen synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; l extracellular matrix degradation inhibitor; mimetope; cirrhosis.
  The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93133
                                                                                                                                 Disclosure;
                                                                                                                                                                                partial
                                                                                                                                                                                                                                                                                                                                         Borras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200031135-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transforming growth
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             The present sequence is a peptide encoded by one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis.
                                                                                    The present invention relates to oligonucleotides (see AAL26793-AAL34 encoding polymorphic variants of proteins related to amylases, amylois proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, cinterferons, interleukins, G-protein coupled receptors and thioesteral proteins.
                                                                                                                                                                                                                                        Polymorphic nucleic acids encoding oncogenes and histones, useful for
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27-DEC-2000;
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interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is a peptide encoded by one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amyloid protein; angiopoletin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factu complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease.
                                                                                                                                                                                                                                                                                                                   The present invention relates to oligonucleotides (see ALI26793-AALI34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoletin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, complement related proteins, cytochromes, kinesins, cytokines,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic nucleic acids encoding e.g. amylases, oncogenes and histones, useful for diagnosing and cancer, autoimmune diseases and infections -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grave's disease), inflammation, cancer (e.g. cancers of the bladder, in, breast, colon and kidney, leukaemia), diseases of the nervous tem and an infection of pathogenic organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-465210/50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0173419
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Pred. No. 2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cyclins, polymerases, treating, e.g.
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1 SLDA 4

Query Match Best Local S Matches

Similarity

100.0%;

Score 18; DB Lo; Pred. No. 2.4e+02;

Length

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Indels

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Gaps

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Conservative

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RESULT 33
AAR93618
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                                  An antigenic conjugate, useful as a vaccine for AIDS, has the formula (SpNE)n-(OMPC), where SPNE is a selected principal neutralisation epitope of HIV, which is one of 27 specified polypeptides (including the present sequence) or their fragments containing at least 5 amino acids and including the DRW or DKW region; OMPC is purified outer membrane proteosome of Neisseria (pref. N. meningitidis); and n is 1-200, indicating the number of SPNE moieties covalently linked to the OMPC. The conjugates may be substituted by anions, and conjugation may be via a bigeneric spacer. The SPNE polypeptides bind an HIV broadly neutralising monoclonal antibody (2F5 antibody) specific for the ectodomain of HIV gp41 transmembrane glycoprotein. They were originally identified in the screening of phage epitope libraries having the library used was library ALPHA described in AAR83295. The sequences of these polypeptides were deduced from their corresponding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
Sequence
                                                                                                                                                                                                                                                                                    New antigenic conjugate useful as vaccine for AIDS principal neutralisation epitope covalently linked proteosome of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB2282379-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  system and
                                                                                                                                                                                                                                                            Claim 14;
                                                                                                                                                                                                                                                                                                                                                                       Arnold BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV principal neutralisation epitope binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR93618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR93618 standard;
                                                                                                                                                                                                                                                                                                                                                                                               (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                           30-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-1996
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                                                                                                                                                                                                                                                                                                                                            1995-125266/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             selected principal neutralisation epitope; vaccine; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.
                                                                                                                                                                                                                                                          Page 8; 75pp;
                            determined
 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an infection of pathogenic organisms
                                                                                                                                                                                                                                                                                                                                                                       Conley AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0129997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteosome; Neisseria; OMPC; AIDS; 2F5 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                     94GB-0019255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide;
                         bγ
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                            PCR.
                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                       Kessler JA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2F5 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                    comprising HIV outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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AAR36604
ID AAR3660
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                                                                                                                                                                                         The present sequence is that of a D3 peptide derived from human CC inhibits endothelial cell proliferation and thus possesses anti-angiogenic activity. It is an example of D3 peptides of the CC invention (see AAY95405-26) that are analogues of certain sites in CC and in which native cysteine residues may be replaced by alanine CC may also induce endothelial cell apoptosis. Compositions including CC the peptides are used in calamed methods for inhibiting angiogenesis, can indicate the peptides are used in claimed methods for inhibiting angiogenesis, cell apoptosis. Concer, rheumatoid arthritis, and ocular disorders The TC50 value for the present peptide was 42 um for inhibition of the retina are treated. The TC50 value for the present peptide was 42 um for inhibition of the retina are treated.
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AAY95420
                                                                                                                                           Query Match
Best Local
                                                                                                                               Matches
         AAR36604 standard; peptide; 19
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MCCR/) MCCRAE R K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200035407-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue; endothelial cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-angiogenic D3 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy; human; D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-SEP-2000
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                                                                                                                                         Local
                                                                                                    1 SLDA 4
                                                                           SLDA 11
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                                                                                                                             4;
                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                              16 AA;
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              29;
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                                                                                                                                                                                                                                                                                                                                                                                                            44pp;
                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                         0;
                                                                                                                                   Score 18; DB 21;
Pred. No. 2.5e+02;
                                                                                                                         Mismatches
                                                                                                                                             Length 16;
                                                                                                                      Indels
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RESULT 36
AAY91397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                              neuroleptic; antimanic; cerebroprotective; immunomodulatory; anti-microbial; cardiant; cytostatic; antiinflammatory; haemostatic; anti-microbial; cardiant; cytostatic; antiinflammatory; haemostatic; anticonvulsant; vasotropic; vaccine; gene therapy; anti-sense therapy; neural; reproductive; immune disorder; immunodeficiency; infection; lymphoma; demyelinating disease; autoinmunity; cancer; inflammation; aneurysm; haemorrhage; Alzheimer's disease; Parkinson's disease; aneurysm; haemorrhage; Alzheimer's disease; parkinson's disease; mendioniti
                                 aneurysm; haemorrhage; Alzheimer's disease; Parkinson's disease
Huntington's disease; Tourette syndrome; multiple sclerosis;
ischaemia; mania; dementia; obsessive compulsive disorder;
viral prophylaxis; developmental disorder; sexually-linked di
                                                                                                                                                                                                                                                                          Human; secreted protein; diagnosis;
                                                                                                                                                                                                                                                                                                                                       Human secreted
                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY91397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY91397 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              See also AAR36602-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phase protein isolated from bovine serum. The protein provides convenient marker for identifying the presence of infection prict the onset of observable symptoms, esp. in feedlot animals. Seri illnesses may be thwarted and economic losses avoided. The protein provides convenient protein provides convenient protein provides convenient protein provides convenient protein provides protein provides convenient protein prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assay kit for detection and prognosis of infection and tissue damage in mammals - using acute phase proteins identified in bovine subjects suffering from infection or induced tissue damage and their specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-167625/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYSA-) UNIV SASKATCHEWAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence shown is the N-terminal sequence of a se protein isolated from bovine serum. The prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      set of observable symptoms, esp. in feedlot animals. Serious sees may be thwarted and economic losses avoided. The protein for monitering of disease states and to identify contaminated X in the sequence defines an undetermined amino acid residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 23; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Redmond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue damage; assay kit;
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                   disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                            protein sequence encoded by gene 23 SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-0971559
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                food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harland R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18; DB
Pred; No. 3e+
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ĀĀ.
                                                                                                                                                                                                                                                                          neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     marker; bovine
             preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 kD acute
                                                                                                                                                                                                                                                                                                                            NO:118
                                 disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ides a prior to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 37
AAY36691
   KW XEXTX AX
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The polynucleotide sequences given in AAA26281 to AAA26336 encode the human secreted proteins given in AAY91346 to AAY91449. The human secreted proteins can have activities based on the tissues and cells they are expressed in Examples of the activities are: neuroprotective; nootropic; neuroleptic; antimanic; cerebroprotective; immunomodulatory; neuroleptic; antimanic; cerebroprotective; immunomodulatory; anti-microbial; cardiant; cytostatic; antinflammatory; haemostatic; anticonvulsant; and vasotropic. The polynucleotides and proteins may be used to prevent, treat or ameliorate a medical condition, e.g. by protein or gene therapy. Conditions treatable by the proteins of the invention include neural, reproductive, or immune disorders, especially lambunodeficiency, infection, lymphomas, demyelinating diseases, auto-immunities, cancer, general microbial infection, inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aneurysms and haemorrhages. Specific examples include: Alzheimer's disease; Parkinson's; Huntington's; Tourette syndrome; multiple sclerosis; meningitis; ischaemia; prostate cancer; mania; dementia; obsessive compulsive disorder and viral prophylaxis. The polynucleotides and proteins can also be used in the detection of disorders associated with the function of the protein, for example, the detection of developmental disorders, sexually-linked disorders, or disorders of the cardiovascular system. They may also be used as food additives or preservatives. AAA26272 to AAA26280 and AAV91345 are sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moore PA,
Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 383; 416pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel secreted proteins and corresponding DNA molecules that can be used to prevent, treat and diagnose disease in humans, for example, Alzheimer's, cancer, and immune disorders -
Human; secreted protein; cancer; tumour; developmental abnormality;
foetal deficiency; blood disorder; immune system disorder; inflammation;
autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
                                                                         Fragment of human secreted protein encoded by gene 57.
                                                                                                                    17-SEP-1999
                                                                                                                                                        AAY36691;
                                                                                                                                                                                          AAY36691 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-AUG-1998;
31-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200011014-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                      1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-224656/19
                                                                                                                                                                                                                                                                                                                                                                  4.
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Lafleur DW, Endress GA, El
                                                                                                                                                                                                                                                                                                                                                                                                                                             19 AA;
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0097917.
98US-0098634.
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                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 21; Length 19;
Pred. No. 3e+02;
Nismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t, Rosen CA,
Ebner R, Kor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA, Florence KA;
Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                                  0;
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AAR33356 ID AAR XX

AAR33356 standard;

peptide;

21

RESULT 38

В

14

1 SLDA 4 SLDA 17

Matches Query Match

Local Similarity les 4; Conserv

Conservative

0;

100.0%;

Score 18; Pred. No. Mismatches

3.2e+02; DB 20;

Length 20; Indels

0,

Gaps

0;

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AXY AAX97916 to AAX98029 represent 110 isolated human secreted protein CC genes. AAY36224 to AAY36727 represent the secreted proteins encoded by the 110 human genes. The genes and their corresponding secreted CC polypeptides are useful for preventing, treating or ameliorating medical CC conditions, e.g. by protein or gene therapy. Also pathological conditions CC can be diagnosed by determining the amount of the new polypeptides in a CC sample or by determining the presence of mutations in the new genes. CC specific uses are described for each of the 110 genes, based on which CC tissues they are most highly expressed in, and include developing CC products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foetal deficiencies, blood disorders, developmental CC immune system, autoimmne diseases, inflammation, allergies, Alzheimer's CC and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis, CC sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular CC disorders, kidney disorders, digestive/endocrine disorders, infections CC and AIDS. The polypeptides are also useful for identifying their binding CC partners. The sequences given in AAX97907 to AAX97915 and AAY36223 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carter KC, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-1997;
18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yu G;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 522; 537pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated human genes encoding secreted polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-418749/35.
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18-DEC-1997;
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18-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-DEC-1998;
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19-DEC-1997;
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Rosen CA, Ru
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i, Greene JM, Jan
en CA, Ruben SM,
20
ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENOME SCI INC
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97US-0068053.
97US-0068054.
97US-0068064.
97US-0068169.
97US-0068169.
97US-0068367.
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M, Janat F, Kyaw H, Moore
Den SM, Shi Y, Soppet DR, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Florence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorder;
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RESULT 39
ABB51179
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Best Local S
Matches 4
        neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary; antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder; multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer; human immunodeficiency virus; hyperproliferative disorder; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                              A cis-regulatory element required for virion associated protein VP16 mediated induction of herpes simplex virus 1 (HSV1) immediate early (IE) genes consists of three imperfect repeats of the purine-rich interaction with the purine-rich repeats (GA repeats) has been identified in soluble preparations of rat liver nucleic. This GA binding protein (GABP) consists of two separable subunits. Applicants have isolated cDNA clones encoding both subunits of GABP and have revealed that one (GABP alpha) is related to the Ets series of 33-amino acid repeats related in sequence to a variety
                                                           Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV; dermatological; immunosuppressive; antiinflammatory; immunostimulant; cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological;
                                                                                                                    Human secreted protein encoded by gene 176 SEQ
                                                                                                                                                                                                     ABB51179 standard; Protein; 26
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding GA binding protein sub-unit - allows investigation of sub-unit sequence motif functions, for control of rapid cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             division e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CARN-) CARNEGIE INST WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09304166-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GA binding protein; cis-regulatory element; VP16 mediated induction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of tryptic peptide derived form purine-rich repeat (GA repeat) binding protien (GABP) at peale 5.
                                                                                                                                                                                                                                                                                                                              Local Similarity les 4; Conserv
                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                            proteins.
                                                                                                                                                                                                                                                                                        SLDA 4
    disease;
                                                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 4; 68pp;
                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mc Knight
                                                                                                                                                                                                                                                                                                                                                                                 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                            0.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thompson
                                                                                                                                                                                                                                                                                                                                          Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                         ; DB 14;
. 3.4e+02;
ches 0;
                                                                                                                       ID NO:1132
                                                                                                                                                                                                                                                                                                                                                    Length
syndrome;
                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 40
AAU88904
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                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              dermatological; immunosuppressive; antinflammatory; immunostimulant; anti-HIV; cytostatic; cardiant; anti-angiogenic; ophthalmological; neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular; antiparkinsonian; antimicrobial; and vulnerary (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) can be used in the prevention, diagnosis and treatment of immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immunodeficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiomyopathy and coronary arteriosclerosis, angiogenic charge's cardiomyopathy and coronary arteriosclerosis, angiogenic retinopathy), neurological disorders (e.g. tuntington's chorea,
                             18-JUN-2002
                                                                                       AAU88904 standard;
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                             retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to ABA83193 and ABB50300 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activities based Example of these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding 207 human secreted polypeptides, useful for preventing, diagnosing and/or treating, e.g. cancers, Parkinson's disease and diabetic retinopathy - |
                                                                                                                                                                                                                                                                                                                           the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-625724/72.
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Florence C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-FEB-2000;
29-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chaga's cardiomyopathy; coronary arteriosclerosis; anglogenic dicorneal graft neovascularisation; diabetic retinopathy; regenera neurological disorder; Huntington's chorea; Alzheimer's disease; Parkinson's disease; infectious disease; chromosome 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-AUG-2001
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                                                                                                                                                                                                   1 SLDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to ABB51287 and ABA83194 to ABA83441 represent human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Hu J, I
Endress GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           er R, Lafleur DW, Moore PA, Olsen H
Soppet DR, Young PE, Shi Y, Floren
Soppet DR, Young PE, Shi Y, Floren
L, Hu J, Li Y, Kyaw H, Fischer CL,
                                                                                                                                                                                                                                                                                               26
                                                                                                                                                                                                                                    Conservative
                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
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2000US-193170P.
                                                                                                                                                                                                                                                                                               AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotide (II) sequences. (I) and (II) have var on the tissues and cells the genes are expressed in activities include: immunomodulatory; antisclerotic.
                                                                                       Peptide;
                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1533pp; English.
                                                                                       26
                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                             Score 18; DB
Pred. No. 4.2
0; Mismatches
                                                                                                                                                                                                                               4.2e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y, Florence KA, Wei .
TL, Ferrie AM,
                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       various
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Insulin/insulin-like growth factor

receptor-binding peptide #860.

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RESULT 41
AAW10854
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 Query Match
                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                          mammalian cells by administering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site 1 of IR and an insulin agonist are useful for treating diabetes. Also, peptides that are useful for treating diabetes. Also, peptides that are useful for treating diabetes. Also, peptides that are useful for treating agrowth factor (IGF-1) receptor are useful for treating insulin-like growth factor (IGF)-sensitive tumours (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1 receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful therapeutics and research reagents. AAU88034-AAU90957 represent IR and/or IGF-1 receptor-binding peptides and related amino acid access.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; antidiabetic; neuroprotective; cerebroprotective; ophthalmological; insulin; receptor; gene therapy; diabetes; insulin-like growth factor-1; IGF-1; tumour; prostate; breast; insulin-tite growth; neurological diseases; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetic neuropathy.
          Functional surrogate; analyte; affinity receptor; immunoreactive group; mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia; cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin; pregnancy; infectious disease; ferritin; myosin light chain; troponin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Figure 1K-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetes and insulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200172771-A2
pregnancy; infectiou follicle stimulating
                                                                                                                    07-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modulating insulin activity in mammalian cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beasley J,
Brissette R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-2000; 2000WO-US08528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-2000; 2000WO-US08528
                                                                                                                                                 AAW10854
                                                                                                                                                                           AAW10854 standard; peptide;
                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                              1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                   the invention.
                                                                                                                                                                                                                                                    SLDA
                                                                                                                                                                                                                                                                                                            4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGI BIOTECHNOLOGIES LLC. NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                      26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blume AJ, Schaeffer
, Spetzler J, Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ravera M,
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumours, comprises using
growth factor receptors
                                                                                                                 (first entry)
                                                                                       binder
                                                                                                                                                                                                                                                                                                                       100.0%;
 hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprises using
                                                                                    sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hsiao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390pp; English
                                                                                                                                                                            29
                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ~
                                                                                                                                                                                                                                                                                                         Score 18; DB 23;
Pred. No. 4.2e+02;
; Mismatches 0;
                                                                                                                                                                            A
                                                                                     FC11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Σŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pillutla R,
Ostergaard S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nan cells, for treating peptides that bind to i
                                                                                     from R26 library
                                                                                                                                                                                                                                                                                                                                     Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brandt
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mandecki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               j e.g.
insulin or
                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                            0;
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AAR71050
ID AAR7
XX
AC AAR7
XX
DT 15-1
XX

15-NOV-1995 AAR71050; AAR71050

(first entry)

Вþ

10

1 SLDA 4 SLDA 13

Matches Query Match

Local

Similarity 4; Conserv

Conservative

0;

Mismatches

100.0%;

Score 18; Pred. No.

4.8e+02; DB 18; 0

Length 29;

0;

Gaps

0

RESULT 42

standard;

Peptide;

30

B

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This sequence represents a monoclonal anti-hepatitis B antigen binder consequence from the R26 library which may be used in the conjugate of the convention. The novel labelled conjugate comprises at least one label catached to a functional surrogate comprises at least one label catached to a functional surrogate of an analyte of interest. The conjugate is capable of competing effectively with the analyte for a cativity that is altered upon interaction with the affinity receptor and this activity can be measured and related to the amount of the analyte present in a sample. Functional surrogates such as this have can immunoreactive group that allows the surrogate to compete effectively and with the analyte for a limiting amount of its affinity receptor. They can be labelled for use in standard competitive affinity assays cap you provide a surrogate and receptor.

CC They can be labelled for use in standard competitive affinity assays cap polypoptides, polysaccharides, polynucleotides, glycoproteins and conjugates are able to minic naturally occurring analytes. Typical constaining macromolecules, polynucleotides, glycoproteins and conjugates and conjugates are able to minic naturally occurring analytes.

CC as polypoptides, polysaccharides, polynucleotides, glycoproteins and conjugates and conjugates and conjugates are altered to fertility-pregnancy or analytes associated with infectious disease. In particular, the assays are useful for detecting ferritin, follicle stimulating hormone, human placental conjugates and conjugates and conjugates and conjugates and conjugates are useful for detecting ferritin, follicle stimulating hormone, human placental conjugates and conjugates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prolactin; parathyroid hormone; placental lactogen; hepatitis antigen antibody; chorionic gonadotropin; luteinising hormone; cytomegaloviru Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen; carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
                                                 Chlamydia, Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin, carcinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen and CA125 (a tumour marker).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-077284/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09641172-A1
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CYTO-) CYTOGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ferritin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page
29
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95; 156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0476375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-US10498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      placental lactogen; hepatitis antigen; n; luteinising hormone; cytomegalovirus;
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Draculin

peptide #13

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RESULT 43
AAW31683
ID AAW31
XX AAW31
XX AAW31
XX AAW31
XX 27-M2
XX Clost
XX Clost
XX Clost
XX Food
XX
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                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                            Matches
              Clostridium perfringens food poisoning.
                                                                                                                                                                                                                                                                                                                                                                         of the blood coagulation cascade. The anticoagulant activity is not inhibited by serine protease inhibitors such as PMFS or DFP. The molecular weight of Draculin ranges from 75-90 kD and may be used in treatment of acute myocardial infarction, deep vein thrombosis, pulmonary embolism, unstable angina, transient ischemic attacks, peripheral vascular or bypass occlusions and disseminated intravascular coagluation. These peptide fragments were derived from Draculin by cleavage with chymotrypsin and overlapping peptide fragments were compared to determine the complete amino acid sequence of Draculin.
                                                            Clostridium
                                                                                           27-MAR-1998
                                                                                                                           AAW31683;
                                                                                                                                                     AAW31683 standard; Protein; 30
                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequences given in AAR71038-84 represent peptide fragments derived from the anticoagulant protein, Draculin. Draculin is isolated from the saliva of vampire batts and is distinct from other known anticoagulants in that it inhibits both factors IX and X of the blood coagulation cascade. The anticoagulant activity is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New anticoagulant protein, draculin, from vampi and related nucleic acid, vectors, transformed for treating myocardial infarction, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anticoagulant; Draculin; saliva; vampire bat; inhibition; factor IX; factor X; blood coagulation cascade; serine protease inhibitor; PMFS; acute myocardial infarction; deep vein thrombosis; pulmonary embolism; unstable angina; transient ischemic attack; peripheral vascular; DFP; bypass occlusion; disseminated intravascular coagluation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; Page 34; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-106668/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apitz-Castro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RHON ) RHONE POULENC RORER PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hemker H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09505836-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desmodus rotundus
                                                                                                                                                                                                                                                  1 SLDA 4
                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                   SLDA
                                                                                                                                                                                                                                                                                             4.
                                                                                                                                                                                                                                                                                                                                                       30 AA;
                                                        perfringens type A enterotoxin
                                                                                                                                                                                                                                                                                            Conservative
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0109807.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bequin S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Undefined amino acid"
                                                                                                                                                                                                                                                                                                        100
                              type A
                                                                                                                                                                                                                                                                                     .0%; Score 18; DB 16; .0%; Pred. No. 4.9e+02; ... wismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hemker HC,
                            enterotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from vampire bat saliva - ransformed cells and probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holt JC,
                                                        (residues 291-319).
                         toxoid; vaccine,
                                                                                                                                                                                                                                                                                                                    Length 30;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lynch K;
                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                     0,
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RESULT 44
AAY95418
ID AAY95
XX
 XX DXX
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                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                             Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue; endothelial cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic; therapy; human; D3 peptide; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence corresponds to a carboxy-terminal protein fragment (amino acid residues 290-319) of the Clostridium perfringens type A enterotoxin protein. Plasmids containing E. coli expression vectors and Clostridium perfringens type A enterotoxin gene fragment encoding amino acid residues 171-319 or 290-319 can be used to produce clostridium perfringens type A enterotoxin toxoids. A synthetic peptide corresponding to these residues 290-319 can also be prepared to be used as a toxoid. These toxoids irreversibly bind to and saturate receptor sites on intestinal membranes, thus effectively competing for these receptor sites with Clostridium perfringens type A enterotoxin. The synthetic peptide and the recombinant carboxy-terminal fragment, are useful as toxoids in a vaccine for preventing C. perfringens food poisoning, or in a composition to treat such food poisoning.
16-DEC-1998;
                         02-DEC-1999;
                                                                            WO200035407-A2
                                                                                                       Homo sapiens
                                                                                                                                                                                               Anti-angiogenic D3 peptide.
                                                                                                                                                                                                                           25-SEP-2000
                                                                                                                                                                                                                                                     AAY95418;
                                                                                                                                                                                                                                                                          AAY95418 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Columns 19-20; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA molecule encoding Clostridium perfringens enterotoxin fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-NOV-1990;
22-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium perfringens. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYPI-) UNIV PITTSBURGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5695956-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                              1 SLDA 4
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                                                                                                                                                                                                                                                                                                                                                SLDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC,
                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toxoid in vaccine for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcclane BA,
                                                                                                                                                                                                                        (first entry)
                       99WO-US28465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90US-0618541.
92US-0874982.
94US-0213452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-0213452
                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mietzner TA;
                                                                                                                                                                                                                                                                             32
                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 18;
Pred. No.
                                                                                                                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              . 4.9e+02;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       food poisoning
                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         30;
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Best Local
                                                                                                                                                                                                                                 Functional surrogate; analyte; affinity receptor; immunoreactive group; mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia; cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin; pregnancy; infectious disease; ferritin; myosin light chain; troponin; follicle stimulating hormone; human; growth hormone; immunoglobulin E; prolactin; parathyroid hormone; placental lactogen; hepatitis antigen; antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus; Streptcoccus; rubella; toxoplasma; DK-MB; prostate-specific antigen; carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of a D3 peptide derived from human high mol.wt. kiningen (HK) domain 3 (see AAY95426). The D3 peptide inhibits endothelial cell proliferation and thus possesses anti-angiogenic activity. It is an example of D3 peptides of the invention (see AAY95405-26) that are analogues of certain sites in the HK domain 3, in this case amino acid residues Leu331-Tyr338, where native cysteine residues may be replaced by alanine residues. The peptides inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting angiogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders characterized by undesired vascularization of the retina are treated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain
 Carter JM,
                                                                                                                                                                                                                                                                                                                                                                                                     MAb anti-HBsAg binder sequence, FC11, from R26 library.
                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW10869 standard; peptide; 33 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 29; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 analog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-442247/38
                                                                    07-JUN-1995;
                                                                                                                                                                  WO9641172-A1
                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCrae RK;
                                                                                                                                    19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UTEM ) UNIV TEMPLE.
(MCCR/) MCCRAE R K.
                                 (CYTO-) CYTOGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 SLDA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 AA;
   Lee-Own FV;
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                    95US-0476375
                                                                                                   96WO-US10498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; 5c.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18; DB 21;
Pred. No. 5.3e+02;
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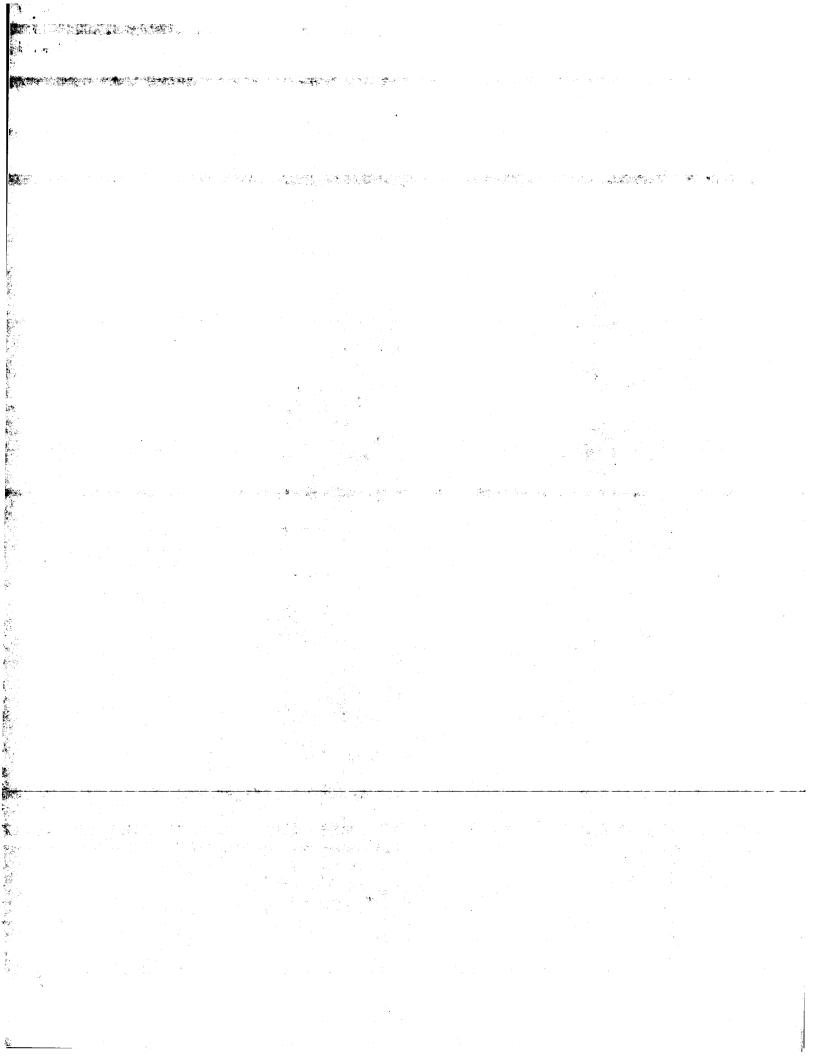
14 SLDA 17

Search completed: February Job time: 29.8333 secs

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2003, 11:19:40

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CC and with the analyte for a limiting amount of its affinity receptor. CC Functional surrogates are able to mimic naturally occurring analytes. CC Functional surrogates are able to mimic naturally occurring analytes. CC Functional surrogates are able to mimic naturally occurring analytes. CC (sep. homogenous immunoassays) for detecting large macromolecules such cas polypeptides, polysaccharides, polynucleotides, glycoproteins and CC lipid-containing macromolecules, as well as small haptens. Typical cdiagnostic analytes for detection include cardiac or tumour markers, CC diagnostic analytes for detection include cardiac or tumour markers (CC allergens, hormones related to fertility-pregnancy or analytes associated CC with infectious disease. In particular, the assays are useful for CC tummunoglobulin E, prolactin, parathyroid hormone, human growth hormone, CC immunoglobulin E, prolactin, parathyroid hormone, human growth hormone, CC chorionic gonadotropin, human luteinising hormone, cytomegalovirus, CC chamydia, Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, CC myoglobin, myosin light chain, troponin, carcinoembryonic antigen, antigen, prostate-specific antigen and CA125 (a tumour marker).
                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a monoclonal anti-hepatitis B antigen binder sequence from the R26 library which may be used in the conjugate of ti invention. The novel labelled conjugate comprises at least one label attached to a functional surrogate of an analyte of interest. The surrogate is capable of competing effectively with the analyte for a surrogate is capable of competing effectively with the analyte for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 51; Page 100; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      such as ferritin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules
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                                                                                                                                                            Sequence
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Perfect score:
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-08-426-985-12
US-08-226-985-12
US-08-246-5313-96
US-08-461-598-96
US-08-322-137-96
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Query Match Best Local Matches	RESULT 1 US-08-136-743B-48 Sequence 48, Applicat 59063 Patent No. 5459063 Patent No. 545901 Patent No. 54590 Patent No. 54590 Patent No. 5459 Patent No. 54		
h Simi 4;	IT 1 Continue Con		
100 Similarity 100 4; Conservative	UECANT SAPELICATION US/08136743 UERAL INFORMATION: APPLICANT: BARRY S. Cooperman, HAPPLICANT: THE UNIVERSION: The Total of INVENTION: Thereof Red TITLE OF INVENTION: THE UNIVERSET: 3700 MARKET STREET: 3700 MARKET STREET: 3700 MARKET STREET: 3700 MARKET STREET: WILLIAM STATE: Pennsylvania COUNTRY: U.S.A. ZIT: 19104-3246 COUNTRY: U.S.A. ZIT: 19104-3246 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 in COMPUTER: IBM PS/2 OPERATION SYSTEM: MS-DOS SOFTWARE: WORDERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION UNMBER: 30,480 REGISTRATION NUMBER: 30,480 REGISTANTION NUMBER: 30,740 REG		1000.0000.0000.0000.0000.0000.0000.000
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RESULT 4
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                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1996-1
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Patent No. 60300.
Patent No. 60300.
Patent No. 60300.
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CURRENT FILING DATE: 1998-03-17
EARLIER APPLICATION NUMBER: 08/919,748
EARLIER FILING DATE: 1997-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PEPTIDES, PEPTIDE ANALOGS, PEPTIDOMIMETICS TITLE OF INVENTION: SMALL MOLECULES USEFUL FOR INHIBITING THE TITLE OF INVENTION: REGOUCLEOTIDE REDUCTASE
                                                                                                                                                                                            ORGANISM: Mycobacterium tuberculosis strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 61 SOFTWARE: Patentin Ver. 2.0
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EARLIER FILING DATE: 1996-08-30
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                                                                                                                        Conservative
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                                                                                                                                                                                                         SOFTWARE: PatentIn Relections of the control of the
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APPLICANT: Hu, Weiming
TITLE OF INVENTION: Gene
TITLE OF INVENTION: in I
FILE REFERENCE: 008103/1
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                                                      REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 43, CITY: San Diego
CTATE: California
"nited St
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ruoslahti, I
APPLICANT: Pasqualini,
TITLE OF INVENTION: Met
TITLE OF INVENTION: Hor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE LOCATION: (1)...
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                           TELEPHONE:
                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
COMPUTER: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: (ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2, Application US/08526710 5622699
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(619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States
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                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruoslahti, Erkki
                           (619) 535-9001
                                                                                                                                                                                                                                                        11-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          )N: in Plants
008103/195497
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Home to a Selected Organ In Vivo
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Colleen
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Pred! No. 1.9e+05;
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GENERAL INFORMATION:
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Best Local 9
                                                                                   Query Match
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APPLICATION NUMBER: US 08/526,710

FILLING DATE: 11-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/813,273

FILLING DATE: 10-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REGISTRATION NUMBER: 31,815
                                                                                                                                                                       TELEFAX: (619) 535-8949
NFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California
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4370 La Jolla Village Drive, Suite 700
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                                                        Conservative
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                                                   Score 18; DB 3, Pred. No. 1.9e+05;
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Pred. No.
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RESULT 7

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RESULT 8
US-09-227-906-12
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Best Local
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                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 01 FILING DATE: 11-SEP-1995 PRIOR APPLICATION DATA:
                                                                                                                           APPLICANT: Ruoslahti, I
APPLICANT: Pasqualini,
TITLE OF INVENTION: Mei
TITLE OF INVENTION: Ho
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APPLICATION NUMBER:
STREET: STREET STREET STREET SAN Diego CITY: San Diego California United St
                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
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CORRESPONDENCE ADDRESS:
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APPLICANT: Pasqualini, Rena
                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/813,273 FILING DATE: 10-MAR-1997
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CITY: San Diego
STATE: Californi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/226,985
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                                                       E: Campbell & Flores LLP 4370 La Jolla Village Drive, Suite 700
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4370 La Jolla Village Drive, Suite 700
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ilarity 100.0%;
Conservative 0
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                                                                                                                               Home to a
                                                                                                                                              Method of
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Pred. No.
                                                                                                                           Identifying Molecules That Selected Organ In Vivo
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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MEDIUM TYPE:

READABLE FORM:

Floppy disk

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                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
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APPLICATION NUMBER: US 08/526,710

FILING DATE: 11-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION USBER: US 08/813,273

FILING DATE: 10-MAR-1997

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                      APPLICANT: TRUEHEART, JOSHUA
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES,
NUMBER OF SEQUENCES: 119
                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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REFERENCE/DOCKET NUMBER: P-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 01
FILING DATE: 23-MAY-1997
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                      STREET: 419 JULY CITY: Washington
APPLICATION NUMBER: US/0:
FILING DATE: 05-JUN-1995
                                                                                                                                      COUNTRY: UZIP: 20004
                                                                                                                                                                    STATE: D.C.
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RATION NUMBER: 31,815
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                                                                                                                                                                                                  419 Seventh Street, N.W., Suite 300
                                                                                                                                                      USA
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100.0%; Pred. No. 1.
               US/08/464,531
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                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 58/00.
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Best Local Similarity
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                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                APPLICANT: PAUL, Jeremy
APPLICANT: TRUEHEART, Joshua
TITLE OF INVENTION: YEAST CEL
TITLE OF INVENTION: PHEROMONE
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LENGTH: 13 amino acids
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TELEFAX: 202-737-3528
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APPLICATION NUMBER: US 08/322,137 FILING DATE: 13-OCT-1994
                                                          APPLICATION NUMBER: US/08 FILING DATE: 05-JUN-1995
                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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419 Seventh Street, N.W.,
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                                                                          US/08/461,598
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Pred. No. 51;
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APPLICATION NUMBER: FILING DATE: 20-SEP

20-SEP-1994

US 08/190,328

US 08/309,313

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;; TYPE: amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: peptide
US-08-461-598-96
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Best Local Similarity
"~+~hes 4; Conserva
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US-08-322-137-96
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                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPOTER:
COMPUTER: IBM PC COMPOTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,137
FILING DATE: 13-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,313
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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LENGTH: 13 amino acids
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APPLICATION NUMBER:
FILING DATE: 31-JAN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1993
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: YEAST CELLS ENGI
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                               APPLICATION NUMBER: US 0 FILING DATE: 31-JAN-1994
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REFERENCE/DOCKET NUMBER:
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419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                     USA
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BROACH, Jim
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31-MAR-1993
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FOLWKES=2F
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Matches
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Matches
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                                                           Query Match
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APPLICANT: Klein, Christine A.
APPLICANT: Murphy, Andrew J. M.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Identifying Receptor Effectors
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-4214
INFORMATION FOR SEQ ID NO: 32:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Catherine J. Kara
                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,33
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                                                                                                                                                      SEQUENCE CHARACTERISTICS LENGTH: 13 amino acids
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
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                                                                                                        MOLECULE TYPE: protein
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                                                                                                                      TYPE: ami
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COUNTRY:
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GY: linear
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                                                                                                                                                                                                                                                                                                                           17-JAN-1996
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                                                                                                                                                                                                                                                                41,106
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                                                                                                                                                                                                                                                   CPI-012CP5
                                              Score 18; DB Pred. No. 51;
                              Mismatches
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                              0;
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                              Indels
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US-08-887-534A-94
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Best Local Similarity
Watches 4; Conserve
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                                                                                                                                                                                                            RESULT 14
                                                                                                                             Sequence 94, Application US/08887534A Patent No. 6455323
GENERAL INFORMATION:
APPLICANT: Holden, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5695956
GENERAL INFORMATION:
APPLICANT: McClan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOULD, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (215) 575-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                           APPLICANT: Holden, David W.
TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS: LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                             CORRESPONDENCE ADDRESS:
                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 30 amino acids
TYPE: amino acid
TYPE: single
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                ADDRESSEE:
                                                                                                                                                                                                                                                          1 SLDA 4
                                  Chicago
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              Illinois
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                                              E: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (215)
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Mietzner, Timothy A.
                                                                                                                                                                                                                                                                                                                         Conservative
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) 575-6015
States of America
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Enterotoxin Toxoid and Methods of Preparation and Use As
Vaccine and Therapeutic Agent
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                                                                                               106
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Pred. No. 1
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Query Match
Best Local Similarity
Thes 4; Conserve
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TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,521
FILING DATE: 08-MAR-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                REFERENCE/DOCKET NUMBER: OHSU 306A TELECOMMUNICATION INFORMATION:
                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MEDIJIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/
SOFTMARE: Patentin Release #1.0;
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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LENGTH: 63 amino acids
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ZIP: 97204
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                          TELEPHONE:
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REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 28341/33996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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Y: US
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Bronner, C. Eric
Baker, Sean M.
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(503)
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                                 (503) 224-6655
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295-6679
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US-08-209-521-20
                                                         Matches
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Best Local S
                                                                                        Query Match
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                                                                                                                                                                                                         TELEFAX: (503) 295-6679
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
REFERENCE/DOCKET NUMBER: OHSU 306.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MAMMALIAN DNA MITITLE OF INVENTION: MMLH1 AND hPMS1
NUMBER OF SEQUENCES: 30
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                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
24 SLDA 27
                                                         Local Similarity les 4; Conserv
                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/209,521 FILING DATE: 08-MAR-1994
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ZIP: 97204
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                             1 SLDA 4
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Y: US
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                                                                                                                                                                                            64 amino acids
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Bollag, Roni J.
                                                         Conservative
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                                                                                                                                                    linear
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                                                                                                                                                               single
                                                      100.0%; So
100.0%; P
ative 0;
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MAMMALIAN DNA MISMATCH REPAIR GENES
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Pred. No. 2.9e+02;
                                                                         Score 18;
Pred. No.
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                                                           Mismatches
                                                           2.9e+02;
hes 0;
                                                                                        DB 2;
                                                                                     Length 64;
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                                                        Gaps
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RESULT 17

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US-08-961-810-130
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                                                                                                                                                                                                                                                                             RESULT 18
                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Liskay,
APPLICANT: Bronner
APPLICANT: Baker,
                                                                                                                                                                                                                             Sequence 1:
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 129, Application US/08961810 Patent No. 6165713
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...ACTERISTICS:
64 amino acids
rYPE: amino acid
STRANDEDNESS: s1-
TOPOLOGY:
1. OLECULF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,810
FILING DATE:
                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: OH TELECOMMUNICATION INFORMATION: TELEPHONE: (503) 224-6655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                           APPLICANT: KOlOdner, Richard D.
TITLE OF INVENTION: COMMODITIONS AND METHODS RELATING TO DNA
TITLE OF INVENTION: MISMATCH REPAIR GENES
NUMBER OF SEQUENCES: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND METHOTITLE OF INVENTION: MISMATCH REPAIR GENES NUMBER OF SEQUENCES: 134
                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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STREET:
CITY: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (503) 295-6679
TELEX: 360619
                                                                                                                                                                                                                                                                                                                           24 SLDA 27
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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STREET: 5
                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                              130, Application US/08961810
). 6165713
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             E: Heuser
520 S.W.
                                                                                                                                                           Liskay, Robert M.
Bronner, C. Eric
Baker, Sean M.
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Baker, Sean M.
                                                                                                                                                                                                                                                                                                                                                                                              100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                              Bollag, Roni J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heuser
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             Yamhill Street, Suite 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOSITIONS AND METHODS RELATING TO DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Richard D.
                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 4;
Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

STATE: (

Oregon Y: U.S.A.

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RESULT 19
US-08-352-902D-129
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LENGTH: 64 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: $ingliant
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Best Local Similarity 100.
Watches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 129, Application US/08352902D Patent No. 6191268
GENERAL INFORMATION:
                    COUNTRY U.S.A.

ZIP: 97204

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/352,902D
FILING DATE: 09-Dec-1994
CLASSIFICATION: CUnknown
ATTORNEY/AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
NAME: Van Rysselberghe, Pierre C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: OH TELECOMMUNICATION INFORMATION: TELEPHONE: (503) 224-6655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 SLDA 27
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO DNA MISMATCH REPAIR GENES
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Liskay, Robert M. Bronner, C. Eric
                                                                                                                                                                                                                                                                                                                  STREET: 520 S.W. Yamhill Street, Suite 200
                                                                                                                                                                                                                                                                                                         CITY: Portland
             REFERENCE/DOCKET NUMBER: OHSU 306B
                                                                                                                                                                                                                                                                                      STATE: Oregon
                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baker, Sean M.
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100.0%; Pred. No. 2.9e+02;
... Mismatches 0;
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US-08-352-902D-130
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US-08-352-902D-130
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      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 130, Application US/08352902p Patent No. 6191268
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557

REFERENCE/DOCKET NUMBER: OHSU 306B
TELEPHONE: (503) 224-6655
TELEPHONE: (503) 224-6679
TELEFAX: (503) 295-6679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 SLDA 27
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                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 130:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release:#1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/352,902D
FILING DATE: 09-Dec-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO DNA
MISMATCH REPAIR GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Liskay, Robert M.
                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                  LENGTH: 64 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 97204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 520 S.W. Yamhill Street, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Oregon
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100.0%; Score 18; DB 4; llarity 100.0%; Pred. No. 2.9e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 18; DB 4; ilarity 100.0%; Pred. No. 2.9e+02; Conservative 0; Mismatches 0;
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Bollag, Roni J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IE: (503) 224-66
(503) 295-6679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 - 6655 -
                                        DB 4; Length 64;
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Indels

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Gaps

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24 SLDA 27

1 SLDA 4

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RESULT 22
US-08-798-897-16
; Sequence 16, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
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US-08-469-260A-33
                                                                                                                          밁
                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-469-260A-33
                                                                                                                                                                                          Matches
                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33,
                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 708-938-2623 INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 55
TELECOMMUNICATION INFORMATION: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COPPUTER: DESTRICT PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
CITY: A
                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 708-938-2623
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                                                                                                                         58 SLDA 61
                                                                                                                                           1 SLDA 4
                                                                                                                                                                                        Local Similarity
les 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60064-3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08469260A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOHN N. SIMONS
TAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
                                                                                                                                                                                                                                                                                                                                73 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                      100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISA K. MUSHAHWAR
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                                                                                                                                                                                        0,
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                                                                                                                                                                                                    Score 18; DB 4;
Pred. No. 3.4e+02;
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                   Length 73;
                                                                                                                                                                                        Indels
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US-08-978-523-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/08978523 Patent No. 5883229 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS; not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Guastella, J
TITLE OF INVENTION: Gen
TITLE OF INVENTION: Hor
TITLE OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
FILING DALL.

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/798,897

APPLICATION NUMBER: February 11, 1997
                                                                                                                                  ZIF: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: DC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
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TITLE OF INVENTION: Genes (
TITLE OF INVENTION: Homoloc
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                       STATE: I
                                                                                                 APPLICATION NUMBER: UP
FILING DATE: herewith
                                                                                                                                                                                                                                                                                                       STREET: 1100 New CITY: Washington
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                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Guastella, John
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                                                                                                                                                                                                                                                                                                                                              KESSLER, GOLDSTEIN & FOX P.L.L.C.
                                                                                                                    US/08/978,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16:
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Pred. No. 3.9e+02;
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Sequence 59, Application US/09186276B
Patent NO. 6388173
GENERAL INFORMATION:
APPLICANT: Benfey, Philip
APPLICANT: Benfey, Philip
APPLICANT: Mysocka-Diller, Joanna
APPLICANT: Mysocka-Diller, Joanna
APPLICANT: Malamy, Jocelyn E.
APPLICANT: Malamy, Jocelyn E.
APPLICANT: Helariutta, Yrjo
TITLE OF INVENTION: Scarecrow Gene, Promoter and Use
FILE REFERENCE: 5914-075-99
CURRENT APPLICATION NUMBER: US/09/186,276B
CURRENT FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 08/842,445
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US-09-134-001C-3985
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LENGTH: 85
TYPE: PRT
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APPLICANY: Lynn Doucette-Stamm et al
APPLICANY: Lynn DOUCETTE ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3985, App
Patent No. 6380370
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Staphylococcus epidermidis-09-134-001C-3985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                        26 SLDA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 SLDA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 100.0%;
Local Similarity 100.0%;
nes 4; Conservative 0
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STRANDEDNESS: not
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                                                                                                                                                                                                                                                                                                                                                                               1 SLDA 4
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linear
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Pred. No.
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Pred. No.
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                                                                          Uses Thereof
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; LOCATION: (1)...(90)
; OTHER INFORMATION: Xaa =
US-09-186-276B-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 59
LENGTH: 90
TYPE: PRT
           GENERAL INFORMATION:
APPLICANY: Benfey et al.
TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 5914-074-999
CURRENT ETLING NUMBER: US/09/186,188B
CURRENT FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 08/842,445
PRIOR APPLICATION NUMBER: 08/842,445
PRIOR APPLICATION NUMBER: 08/842,445
PRIOR FILING DATE: 1997-04-24
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Best Local S
Matches 4
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 59
LENGTH: 90
                                                                                                                                                                            Sequence 59, Application US/09186188B Patent No. 6455672
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Best Local
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Benfey et al.
TITLE OF INVENTION: Scarcerow Gene, Promoter and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 5914-056-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 08/638,617
EARLIER FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/08/842,445A CURRENT FILING DATE: 1997-04-24
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PRIOR APPLICATION NUMBER: 08/638,617
PRIOR FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 79
PRIOR APPLICATION NUMBER: 08/638,617
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT
LOCATION: (1)...(90)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Oryza sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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o. 6441270
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Pred. No. 4.2
0; Mismatches
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; NAME/KEY: VARIANT
; LOCATION: (1)...(90)
; OTHER INFORMATION: Xaa - Any Amino Acid
US-09-186-188B-59
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US-08-936-165A-515
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 59
LENGTH: 90
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                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION DATA: 60/027,032
APPLICATION UNBER: 60/027,032
APPLICATION NUMBER: 36
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEPAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Plant
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ward, Judith
APPLICANT: Ward, Judith
TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
TITLE OF INVENTION: Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: King of Prussia
STATE: PA
                   LENGTH: 105 amino act
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 SLDA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reichard, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lonetto, Michael
Nicholas, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosenberg, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pratt, Julie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hodgson, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burnham, Martin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Knowles,
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                     515:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18; DB 4;
Pred. No. 4.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PAT
; ORGANISM: Homo sapiens
US-09-099-041A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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Best Local Similarity
"~+~hes 4; Conserv?
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US-09-099-041A-6
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                                                                             US-09-199-637A-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-199-637A-231
                                                                                                                                             PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 231
FERCENT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bertin, C
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Best Local Similarity
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                                         Query Match
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-076001
CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-08-09,041A
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR FILING DATE: 1998-02-06
                                                                                                                                                                                                                                                                        APPLICANT: Drenkard, Eliana
APPLICANT: Tsongalis, John
TITLE OF INVENTION: VIRILENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
                                                                                                                 LENGTH: 10
TYPE: PRT
                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                              ORGANISM: Pseudomonas aeruginosa
r MaiCn 100.0%; Score 18; DB 4; Local Similarity 100.0%; Pred. No. 5.2e+02; hes 4; Conservative 0: Mismatcher.
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o. 6355411
                                                                                                                                      109
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                                                                                                                                                                      FastSEQ for Windows Version 4.0
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Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
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                                         Length 109;
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   Indels
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Matches

0;

Gaps

0;

20

SLDA

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CURRENT APPLICATION NUMBER: US/09/207,359B CURRENT FILING DATE: 1998-12-08 PRIOR APPLICATION NUMBER: US 09/099,041 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: US 09/019,942 PRIOR FILING DATE: 1998-02-06 NUMBER OF SEQ ID NOS: 47 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6
                                                                           B
RESULT 33
US-09-437-054A-2
                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-207-359B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-207-359B-6
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-281-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/245,281
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: US 09/099,041
EARLIER FILING DATE: 1998-06-17
EARLIER APPLICATION NUMBER: US 09/019,942
EARLIER FILING DATE: 1998-02-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09207359B
Patent No. 6469140
GEMERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-112001
                                                                                                                                                 Matches
                                                                                                                                                                                  Query Match
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 07334/118001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                       29 SLDA 32
                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 SLDA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 100.0%;
Local Similarity 100.0%;
                                                                                              1 SLDA 4
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                                                                                                                                                 Conservative
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                                                                                                                                                              100.0%;
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Pred. No. 5
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Pred. No. 5.2e+02;
                                                                                                                                             Mismatches
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                                                                                                                                                                                DB 4;
                                                                                                                                                             .3e+02;
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                                                                                                                                         0;
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                                                                                                                                         Gaps
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; LOCATION: (85)
US-09-437-054A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5834309
Patent No. 5834309 5710045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 114
                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                               APPLICATION NUMBER: US/08/
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Allen, Stephen M.
APPLICANT: Kinney, Anthony J.
TITLE OF INVENTION: Plant Alpha-Glucosidase II Homologs
FILE REFERENCE: BB1273 US NA
CURRENT APPLICATION NUMBER: US/09/437,054A
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/107,909|
PRIOR FILING DATE: 1998 No. 6316698ember-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09437054A Patent No. 6316698
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SOFTWARE: microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS |
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thompson, Craig B. B. APPLICANT: Boise, Lawrence H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: Un
ZIP: 77210
                                                                                                                         REFERENCE/DOCKET NUMBER: ARCD:090--1
                                                                                                                                         NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
               LENGTH:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS |
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Pred. No. 5
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US-08-461-511A-15
; Sequence 15, Application US/08461511A
; Patent No. 6303331
; GENERAL INFORMATION:
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US-08-470-670A-15
                                                                                                                                               RESULT 36
US-09-134-001C-2929
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                                                                                                                                                                                                                                                                                                                                                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: 15: US-08-461-511A-15
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                                                                                                                                                                                                                           В
               GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                            Sequence 2929, Application US/09134001C Patent No. 6380370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-TOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION UNMER: US/08/461,511A

PILING DATE: 05-Jun-1995

CLASSIFICATION UNMER: UNKNOWN

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

REGISTRATION NUMBER: 37,642
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nes 4; Conserv
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                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                              1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: ARCD:179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thompson, Craig B.B.
Boise, Lawrence H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Arnold, Wh. STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                               100.0%;
ilarity 100.0%;
Conservative (
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NUMBER: US/09/134,001C
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Pred. No. 5.
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Pred. No. 5.9e+02;
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                                                                                             ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-213-452-2
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US-08-213-452-2
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SEQ ID NO 2929
LENGTH: 124
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                                  Matches
                                             Query Match
Best Local Similarity
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APPLICANT: McClan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                                                      TELEFAX: (215) 575-601
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE:
                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6010
TELEFAX: (215) 575-6015
                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Gould, Jr., Lewis
REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 424
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                                                                                                                                                        LENGTH:
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 1 SLDA 4
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                                                                                                                                         amino acid
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                                                                                                                                                        149 amino acids
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VENTION: Clostridium perfringens Type A

VENTION: Enterotoxin Toxold and Methods of Preparation and Use As

VENTION: Vaccine and Therapeutic Agent
                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanna, Philip C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McClane, Bruce A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lewis F. Gould, Jr.
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                                             100.0%; Score 18; DB 1; 100.0%; Pred. No. 7.4e+02;
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                                                                                                                                                                                                                                                                     25,057
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Pred. No.
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                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
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                                                            Length 149;
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US-08-606-143-18
                                                                                                                                                                                                                                                  Sequence 16, App. No. 620402
                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local :
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Patent No. 5856155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
STREET: 35.
CITY: Palo Alto
                                                                CORRESPONDENCE ADDRESS:
                                                                                              APPLICANT: Liu, Philip T.
TITLE OF INVENTION: LOW-T
TITLE OF INVENTION: ANALO
                                                                                                                                                                                    APPLICANT:
                                                                                  UMBER OF SEQUENCES:
                                                                                                                                         PPLICANT:
                                                                                                                                                        PPLICANT:
                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 3076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                       53 SLDA 56
                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: lir
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SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                Application US/08954395A
                                    350 Cambridge Ave., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Leydig, Voit & Mayer, Ltd.
Two Prudential Plaza, Suite 4900
                                                                                                                                                Chung, Albert D.
                                                                                                                                                                               Villarete,
                                                                                                                                       Li, Wayne W.
                                                                                                                                                                                            Pontzer, Carol
                                                                                                                                                                                                          Subramaniam, Prem S.
                                                                                                                                                                                                                        Johnson, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                            ANALOG
                                                                                                                                                                   Jackeline
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                                                                                                       LOW-TOXICITY HUMAN INTERFERON-ALPHA
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                                                                                                                                                                                 Lorelie H.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 152;
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US-09-069-023-6
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                                                                  Query Match
Best Local S
                                                      Matches
                                                                                                                                                                    SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                            GENERAL
                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09069023A Patent No. 6348573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/069;023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS TITLE OF INVENTION: SIGNALING PATHWAY, INHIBITORS AND ACTIVATORS FILE REFERENCE: UM-03333
                                                                                                                                                                                 SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                              APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
                                                                                                                                                                                                                                                                                                         APPLICANT: Nunez, Gabriel
                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 27008
REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/6: FILING DATE: 12-APR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
86
                                                                  Local Similarity
                          1 SLDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Dehlinger,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: Filed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                         8 SLDA 11
SLDA
                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                      167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hulfn-alpha analog Ifna-n6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 amino acids
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          650-324-0960
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                                                                  100.0%;
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                                               Score 118; DB 4,
Pred. No. 8.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3e+02;
                                                                           Length 167;
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                                               Gaps
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RESULT

US-08-081-448-8

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US-08-470-670A-9

Sequence 9, Application US/

Patent No. 5834309

Patent No. 5834309 5710045
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                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin ReleacURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE: 19936622
CLASSIFICATION: 424
CLASSIFICATION: 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312-755-4489
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                  ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 312-744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: NO. 5646008thrup, (
REGISTRATION NUMBER: 33, (
REFERENCE/DOCKET NUMBER:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                   TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: TITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Vertebrate Apoptosis Gene: TITLE OF INVENTION: Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thompson, Craig B. APPLICANT: Boise, Lawrence H.
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CITY: C
                                                                                                                                                                                                                                                                                                                                                                                                                                          74 SLDA 77
                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                    COUNTRY: UI
ZIP: 77210
                                                                                                                                                CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100 les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid TOPOLOGY: linear
                                                          MEDIUM TYPE:
                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                       Application US/08470670A
                                                                                                                                    Texas
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                                                                                                                                                    P.O. Box 4433 puston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 amino acids
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321 No. 5646008th Clark Street, Suite 800
                                                                                                                United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                    Thompson, Craig B. B.
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              Release #1.0, Version #1.30
                                                                                                                                                                                                                     18
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US-08-461-511A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-461-511A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08461511A Patent No. 6303331
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (512) 474-75 INFORMATION FOR SEQ ID NO:
                                                                                                       REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:179
TELECOMMUNICATION INFORMATION: (512) 418-3000
TELEPAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 22-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 SLDA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SLDA 4
                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,511A
FILING DATE: 05-Jun-1995
CLASSIFICATION: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
NAME: Highlander, Steven L.
               MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thompson, Craig B.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                       LENGTH: 170 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Houston
                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: P.O. Box 4433
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Pred. No. 8.5e+02;
; Mismatches 0;
                 ID NO:
                 9:
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0;

Query Match

100.0%;

Score 18;

DB 4;

Length 170;

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Sequence 8, Application US/09271014A

Patent No. 6395510

GENERAL INFORMATION:
APPLICANT: THOMESON, CRAIG B.
APPLICANT: BOISE, LAWRENCE H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:316

CURRENT APPLICATION NUMBER: US/09/271,014A

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 8

LENGTH: 170

TYPE: PRT

ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 45
PCT-US94-07089-9
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US-09-271-014A-8
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                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
CURRENT APPLICATION DATA:
APPLICATION UNMBER: PCT/US94/07089
FILING DATE: CONCURRENTLY FILED
CLASSIFICATION DATA:
APPLICATION UNMBER: 08/081.448
FILING DATE: 22 JUNE 1933
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,165
DEFERENCE/DOCKET NUMBER: ARCD090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application PC/TUS9407089 GENERAL INFORMATION:
APPLICANT:
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
                            TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
                                                                     TELEPHONE: 512-320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: VETITLE OF INVENTION: CCNUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Arn
STREET: P.O. B
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                COUNTRY: Un
ZIP: 77210
                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                United States of America
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Compositions and Methods
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; Pred. No. 8.5e+02;
0; Mismatches 0;
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); Mismatches 0;
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В
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Best Local Similarity
Thes 4; Conserve
                                                                                                                            ; TOPOLOGY: 11; ; MOLECULE TYPE: PCT-US94-07089-9
Search completed: February Job time: 10.3333 secs
                                                               Qy
                                           74 SLDA 77
                                                                                                                                                     TOPOLOGY: linear
                                                                1 SLDA 4
                                                                                     100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                         protein
         6,
         2003, 11:24:07
                                                                                     0;
                                                                                  Score 18; DB 5; 1
Pred, No. 8.5e+02;
; Mismatches 0;
                                                                                                      Length 170;
                                                                                  Indels
                                                                                  0;
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Result
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                  Score
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
    /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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    /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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   GenCore version 5.1.3 (c) 1993 - 2003 Compugen
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US-09-758-426-41

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3 US-09-758-128-41

3 US-09-758-128-41

3 US-09-758-128-44

4 US-09-758-128-44

5 US-09-309-196-96

6 US-09-309-196-96

6 US-09-904-615-118

6 US-09-904-615-118

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6 US-09-864-761-35349

6 US-09-727-801-8

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6 US-09-727-801-8
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15.202 Million cell updates/sec
                            Sequence 45, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 10, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 18, Appl
Sequence 118, App
Sequence 118, App
Sequence 118, Appl
Sequence 118, Appl
Sequence 45603, A
Sequence 54, Appl
Sequence 68, Appl
Sequence 68, Appl
Sequence 68, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 8, Appl
                                                                                                                                                                                                                                                                                                                              Description
Sequence 181,
Sequence 267,
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18
100.0	100.0	100.0	100.0	100.0	100.0	100.0	•	100.0	•	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
118	118	109	109	109	109	105	98	98	96	92	92	90	89	86	85	83	81	79	78	77	77	73	70	64	62
10	10	12	10	9	9	10	10	10	10	12	9	10	10	9	10	10	10	10	10	10	10	œ	10	9	10
US-09-867-550-1788	US-09-216-393-58	US-10-105-931-6	US-09-728-721-6	US-09-975-719-231	US-10-118-984-6	US-09-939-980-515	US-09-905-243-49	US-09-905-243-48	US-09-867-550-338	US-10-014-269-21	US-10-002-974-21	US-09-841-879B-10	US-09-931-071-11	US-10-108-605-281	US-09-893-737-56	US-09-925-300-1597	US-09-764-877-1555	US-09-864-761-40746	US-09-764-877-1348	US-09-925-300-1880	US-09-764-869-1073	US-08-424-550B-33	US-09-864-761-34065	US-09-796-692-1225	US-09-864-761-46194
1788	58	Sequence 6, Appli	Sequence 6, Appli	Sequence 231, App	Sequence 6, Appli	Sequence 515, App		Sequence 48, Appl	Sequence 338, App	Sequence 21, Appl	Sequence 21, Appl	10,	Sequence 11, Appl	Sequence 281, App	Sequence 56, Appl	Sequence 1597, Ap	Sequence 1555, Ap	Sequence 40746, A		1880,	Sequence 1073, Ap	Sequence 33, Appl	Sequence 34065, A	Sequence 1225, Ap	Sequence 46194, A

ALIGNMENTS

RESULT 1 US-08-981-824-45

Sequence 4 Patent No.

45, Application US/08981824 o. US20020114816A1

GENERAL INFORMATION:

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APPLICANT: ENDL, JOSEÉ
APPLICANT: STAHL, Peter
APPLICANT: ALBERT, Winfried
APPLICANT: SCHENDEL, Dolores
APPLICANT: BOITARD, Christian
APPLICANT: BOITARD, Christian
APPLICANT: UNG, Gunther-Gerhard
TITLE OF INVENTION: AUTOREACTIVE PEPTIDES FROM
TITLE OF INVENTION: DECARBOXYLASE (GAD)
FILE REFERENCE: 564-7029
CURRENT APPLICATION NUMBER: US/08/981,824
CURRENT FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: PCT/EP96/03093
EARLIER APPLICATION NUMBER: DE/195 25 784.7
EARLIER FILING DATE: 1995-07-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PATENTING DATE: 1995-07-14
SEQ ID NO 45
RESULT 2
US-09-758-426-41
Sequence 41, Application US/09758426
Patent No. US20020169116A1
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Best Local Similarity
"~+~hes 4; Conserv?
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TYPE: PRT
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                                                                                                                                                                              100.0%; Score 18; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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US-09-758-198-41
; Sequence 41, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020187925A1man L.
; APPLICANT: WESTBROOK, Simon L.
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                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Rat
US-09-758-426-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn SEQ ID NO 44
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 016786/0214
CURRENT APPLICATION NUMBER: US/09/758,426
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WESTBROOK, SIMON L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, No. US20020169116Aiman
APPLICANT: WESTBROOK, Simon L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 016786/0214
CURRENT APPLICATION NUMBER: US/09/758,426
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KINGSTON, David J.

APPLICANT: GERRATY, NO. US20020169116Alman L.

APPLICANT: WESTBROOK, Simon L.

TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: AU PN9990 PRIOR FILING DATE: 1996-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 58
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  INVENTION:
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MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
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s 0;
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us-09-997-900-10
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US-09-758-198-44
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                                                                                     GENERAL INFORMATION:
APPLICANT: Kakefuda, Genichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 44, Application US/097 Publication No. US20020187925A1 GENERAL INFORMATION:
                                                                                                                                Sequence 10, Application U
Patent No. US20020053098A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SÖFTWARE: PatentIn Ver.
SEQ ID NO 44
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41
LENGTH: 7
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, No. US20020187925Alman L.
APPLICANT: WESTBROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
                                             APPLICANT:
                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: EARLIER PRIOR FILING DATE: EARLIER FILING NUMBER OF SEQ ID NOS: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/758,198
CURRENT FILING DATE: 2001-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194.
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/0
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/758,198
CURRENT FILING DATE: 2001-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 016786/0214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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                    Sun, Ming
Hu, Weiming
                                                               Costello,
                                                                                                                                                     Application US/09997900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09758198
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                                                                 Colleen
                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: DATE: 1996-05-22
                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                   1.1e+05; thes 0;
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TITLE OF INVENTION: in Plants
FILE REFERENCE: 043753/241148 (5849-20A)
CURRENT APPLICATION UNMBER: US/09/997,900
CURRENT FILING DATE: 2001-11-30

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US-09-758-128-44
; Sequence 44, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
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                                                                             RESULT 8
                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens US-09-758-128-41
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US-09-758-128-41
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LOCATION: (1)..(2)

OTHER INFORMATION: Thrombin cleavage site
US-09-997-900-10
                                                                                                                                                                                       Best Loc
Matches
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PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 09/426,568
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 41, Application US/09758128 Patent No. US20020107187A1
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Best Local Similarity 100
Matches 4; Conservative
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/758,128
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1996-02-05
PRIOR APPLICATION NUMBER: AU PN9990
PRIOR FILING DATE: 1996-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KINGSTON, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, No. US20020107187Alman L.
APPLICANT: WESTBROOK, Simon L.
                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 58
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NAME/KEY: PEPTIDE
LOCATION: (1)..(7)
OTHER INFORMATION: N-terminal
OTHER INFORMATION: of plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Arabidopsis sp.
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TYPE: PRT
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nes 4; Conserv
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Pred. No. 1.1
0; Mismatches
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hes 0;
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1.1e+05;
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RESULT 9
US-09-309-196-96
; Sequence 96, Appl
; Publication No. (
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PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: AU PN9990
PRIOR FILING DATE: 1996-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/758,128
CURRENT FILING DATE: 2001-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                           APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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nes 4; Conservative
                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 419 Seven CITY: Washington STATE: D.C.
              NAME: COOPER, IVER P. REGISTRATION NUMBER: 28 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SLDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09309196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAUL, Jeremy
TRUEHEART, JOSHUA
TRUEHEART, JOSHUA
VENTION: YEAST CELLS ENGINEERED TO PRODUCE
VENTION: PHERMONE SYSTEM PROTEIN SURROGATES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BROACH, Jim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MANFREDI, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MURPHY, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLEIN, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOWLKES, Dana M.
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Pred. No. 1.
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GENERAL INFORMATION:
GENERAL INFORMATION: 49 Human Secreted Proteins
FILE REFERENCE: P2032p1
CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/511,554
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
                                                                                                                                                                                                          US-09-904-615-118
                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: SITE
; LOCATION: (19)
; OTHER INFORMATION: Xaa equals stop translation
US-09-739-254-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                          Sequence 118, Application US/09904615
Patent No. US20020026040A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 4; Conservative
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SEQ ID NO 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 60/097,917
EARLIER FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: 60/098,634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/739,254
CURRENT FILING DATE: 2000-12-19
EARLIER APPLICATION NUMBER: 09/511,554
EARLIER FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: PCT/US99/19330 EARLIER FILING DATE: 1999-08-24
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TITLE OF INVENTION: 49 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: PZ032P1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 19
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TELEFAX: 202-7
TELEX: 248633
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1 SLDA 4
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20010021700A1
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202-737-3528
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Pred. No.
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Pred. No.
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Patent No. US20020048763A1
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LENGTH: 19
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PRIOR APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-x-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Penn, Sharron G.
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PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: SITE
LOCATION: (19)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                       FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
                                                                         APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
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                   FILING DATE: 2000-06-30
                                    FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
                                                                                                        FILING DATE: 2001-01-30
                                                                                                                            APPLICATION NUMBER:
                                                                                                                                             FILING DATE:
                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00661
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                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: GB 24263.6
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Chen, Wensheng
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09/774,203
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NUMBER OF SEQ ID NOS: 49117

SOPTWARE: Annomax Sequence Lii
SEQ ID NO 45603

LENGTH: 34

TYPE: PRT
OGGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRESSED
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US-09-864-761-35349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                                                                                                                FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
                                                                       FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                             ETILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
ETILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
                                                                                                                             FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00661
APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                      APPLICATION NUMBER:
                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00662
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EXPRESSED
                             NUMBER: US 60/234,687
2000-09-21
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Pred. No.
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FETAL LIVER, SIGNAL = 0.77
BRAIN, SIGNAL = 0.7
BONE MARROW, SIGNAL = 0.68
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RESULT 14
US-10-004-717-54
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                                                                                                                                                                              SEQ ID NO 54
LENGTH: 45
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 35349
                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                   NUMBER OF SOFTWARE:
                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE TITLE OF INVENTION: ATOMAL ASSOCIATED SEQUENCE FOR DEAFNESS, TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION FILE REFERENCE: PO1899US4
CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR APPLICATION NUMBER: 60/176,993
PRIOR APPLICATION NUMBER: 60/176,993
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR FILING DATE: 1999-06-01
NUMBER: OF SEQ ID NOS: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ZOGHBI, HU APPLICANT: YANG, QI
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NI EXPRESSED IN BONE MARROW, SIGNAL = 1.4

NI EXPRESSED IN HELA, SIGNAL = 2.2

NI EXPRESSED IN HELA, SIGNAL = 1.3

NI EXPRESSED IN HELA, SIGNAL = 1.3

NI EXPRESSED IN HEALINO, SIGNAL = 1.4

NI EXPRESSED IN LUNG, SIGNAL = 1.6

NI EXPRESSED IN BT474, SIGNAL = 1.7

NI EXPRESSED IN BT474, SIGNAL = 3.7

NI EXPRESSED IN BT474, SIGNAL = 3.7

NI EXPRESSED IN BT474, SIGNAL = 1.7

NI SWISSPROT HIT: P54278, EVALUE 4.00e-16

NI EXPRESSED IN BT474, EVALUE 4.00e-17
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Pred. No.
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Pred. No.
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RESULT 15
US-09-729-674-68
; Sequence 68, Application US/09729674
; Patent No. US20010039335A1
; GENERAL INFORMATION:

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Query Match
Best Local Similarity
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                                                                                   ; NAME/KEY: UNSURE
; LOCATION: (46)
US-09-727-801-8
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US-09-727-801-8
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SOFTWARE: Pate
SEQ ID NO 68
FUNGTH: 50
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SEQ ID NO 8
LENGTH: 53
                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Helentjaris, Tim
TITLE OF INVENTION: Homologs of SCF Ubiquitin-Ligase Complex Component
FILE REFERENCE: BB1418 US NA
CURRENT APPLICATION NUMBER: US/09/727,801
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 60/170377
PRIOR FILING DATE: 1999-12-13
                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09727801 Patent No. US20010034059A1
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NAME/KEY: UNSURE LOCATION: (39)
NAME/KEY: UNSURE LOCATION: (45)
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CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fechtel, Kim-
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: APPLICANT:
                                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
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TYPE: PRT
ORGANISM: Homo sapiens
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Local Similarity 100.0%;
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Spaulding, Vikki
Wong, Gordon G.
Clark, Hilary
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Pred. No.
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SEQ ID NO 34730
LENGTH: 55
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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PRIOR APPLICATION WINDER: US 60/236,359
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                     LENGTH: 55
TYPE: PRT
ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: PCT/US01/00661
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TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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OTHER INFORMATION:
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FILING DATE: 2001-01-30
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Chen, Wensheng
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N BRAIN, SIGNAL = 1.7

N BT474, SIGNAL = 1.4

N HBL100, SIGNAL = 2.1

N HEART, SIGNAL = 2.1

N LUNG, SIGNAL = 2

N ADULT LIVER, SIGNAL = 1

N FETAL LIVER, SIGNAL = 2

IT: P09095, EVALUE 3.40e+
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BONE MARROW, SIGNAL =
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NAL = 2.9
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US-09-764-887-267

; Sequence 267, Application US/09764887

; Patent No. US20020042096A1

; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-887-267
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US-10-001-876-181
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SEQ ID NO 181
LENGTH: 58
TYPE: PRT
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                                                         Matches
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REPERENCE: PALI3
CURRENT APPLICATION NUMBER: US/09/764,887
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and FILE REFERENCE: DEX-0285 CURRENT APPLICATION NUMBER: US/10/001,876 CURRENT FILING DATE: 2001-11-20
                                                                                                                                                                                                     Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 658
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PRIOR FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 211
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APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
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APPLICANT: Macina,
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Pred. No.
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Pred. No. 1.1e+02;
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Pred. No. 1.1e+02;
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; OTHER INFORMATION: US-09-864-761-46194
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                  OTHER INFORMATION: MAP TO ACO24049.2
OTHER INFORMATION: EXPRESSED IN BRAIN
OTHER INFORMATION: EXPRESSED IN PLACE
OTHER INFORMATION: EXPRESSED IN ADJULT
OTHER INFORMATION: EXPRESSED IN FETAL
OTHER INFORMATION: EXPRESSED IN FETAL
OTHER INFORMATION: EXTLUMAN HIT: AAB
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel,
100.0%; ilarity 100.0%; Conservative
                                                                                                                     EXPRESSED IN BRAIN, SIGNAL = 1.6
EXPRESSED IN PLACENTA, SIGNAL = 1.5
EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
EST_HUMAN HIT: AA868675.1, EVALUE 7.00e-31
SWISSPROT HIT: P08980, EVALUE 2.60e+00
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     0;
                          Score 18; DB 10;
Pred. No. 1.1e+02;
       Mismatches
                                                    Length 62;
       Indels
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US-09-864-761-34065
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US-09-796-692-1225
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                                                                                                                                                                                                                                       Sequence 34065, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Versior
SEQ ID NO 1225
LENGTH: 64
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILLING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mandion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
                                                                                                                                                                   APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR
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                                                                                                                                                                                                                                                                                                                                                                       42 SLDA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity les 4; Conserv
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/200,545 FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/190,479 FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/222,903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/218,950 FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/206, 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/202,084 FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/200,303 FILING DATE: 2000-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/223,416
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Pred. No. 1.2e+02;
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US-08-424-550B-33
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 34065
LENGTH: 70
                                                                           Matches
                                                                                                             Query Match
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OTHER INFORMATION: 1
OTHER INFORMATION: 1
OTHER INFORMATION:
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OTHER INFORMATION: MAP
OTHER INFORMATION: EXPI
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TYPE: PRT
11
                                 1 SLDA 4
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FILING DATE: 2001-01-30
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SLDA
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                                                                                           Similarity
                                                                       100.0%; ilarity 100.0%; Conservative (
                                                                                                                                                                                                                                          N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3

N: EXPRESSED IN LUNG, SIGNAL = 0.77

N: EXPRESSED IN HELA, SIGNAL = 1.8

N: EXPRESSED IN PLACENTA, SIGNAL = 1.8

N: EXPRESSED IN PLACENTA, SIGNAL = 0.73

N: EXPRESSED IN BUILT LIVER, SIGNAL = 0.73

N: EXPRESSED IN BRAIN, SIGNAL = 1.4

N: EXPRESSED IN BRAIN, SIGNAL = 1.4

N: EXPRESSED IN BRAIN, SIGNAL = 1.78

N: EXPRESSED IN BRAIN, SIGNAL = 1.78

N: EXPRESSED IN BRAIN, SIGNAL = 1.78
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SWISSPROT
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                                                                                                                                                                 IN BONE MARROW, SIGNAL = 0.78
IN HBL100, SIGNAL = 1.4
HIT: BE746542.1, EVALUE 5.00e-35
HIT: Q15750, EVALUE 4.00e-36
                                                                         0;
                                                                                           Score 18;
Pred. No.
                                                               Mismatches
                                                                                       1.3e+02;
                                                                                                               DB 10;
                                                                                                             Length 70;
                                                                           Indels
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                                                                         0;
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Sequence 33, Application US/08424550B Patent No. US20020119447A1 GENERAL INFORMATION:

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APPLICANT:

JOHN N.

SIMONS PILOT-MATIAS

APPLICANT:

SCHLAUDER

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RESULT 24
US-09-764-869-1073
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APPLICANT: ROSen et al.
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
                                                                                                                                 Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1073
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY, AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELEPHONE: 708-937-6365
TELEPHONE: 708-938-2623
                                                                                                                                                                                                                                                                                                                                                              Sequence 1073, Application US/09764869 Patent No. US20020061521A1
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APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-B. NON-C, NO
TITLE OF INVENTION: REAGENTS AND METHODS FO
NUMBER OF SEQUENCES: 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
FEATURE:
NAME/KEY: SITE
LOCATION: (26)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60064-3500

ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: 100 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100 nes 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ABBOTT PARK
STATE: IL
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100.0%; Pred. No. 1
tive 0; Mismatches
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                                                                 ; NAME/KEY: SITE ; LOCATION: (28) ; LOCATION: (28) ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-877-1348
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US-09-764-877-1348
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US-09-925-300-1880
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                                                                                                                           Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1348
LENGTH: 78
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity 100.
Thes 4; Conservative
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
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LENGTH: 77
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 1348, Application US/09764877 Patent No. US20020147140A1
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                              Query Match
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CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/764,877 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILTNG DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US00/05988 PRIOR FILING DATE: 2000-03-08
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Craig Rosen, APPLICANT: Steve Ruber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE LOCATION: (36)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Local Similarity tes 4; Conserv
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                 100.0%; Score 18; 100.0%; Pred. No.
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Pred. No.
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Pred. No.
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               1.5e+02;
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                                Length 78;
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: Annomax Seque
SEQ ID NO 40746
LENGTH: 79
TYPE: PRT
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                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                    FEATURE:
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PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                             INFORMATION:
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      NFORMATION:
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D. US20020048763A1
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k, David R.
zel, David K.
N: MAP TO AL138796.2

N: EXPRESSED IN ADULT LIVER, SIGNAL = 0.86

N: EXPRESSED IN BRAIN, SIGNAL = 0.86

N: EXPRESSED IN PLACENTA, SIGNAL = 0.64

N: EXPRESSED IN FETAL LIVER, SIGNAL = 0.54

N: EXPRESSED IN HORE MARROW, SIGNAL = 0.55

N: EXPRESSED IN HEART, SIGNAL = 2.6

N: EXPRESSED IN HEART, SIGNAL = 2.6

N: EST_HUMAN HIT: H29179.1, EVALUE 2.00e-21

N: SWISSPROT HIT: P21179, EVALUE 3.30e+00
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RESULT 29
US-09-925-300-1597
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US-09-764-877-1555
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Best Local S
SOFTWARE: PatentIn Ver.
SEQ ID NO 1597
LENGTH: 83
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APPLICANT: Rosen et al.
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                                                                             CURRENT APPLICATION NUMBER: US/09/925, 300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
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Best Local (
                                       PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
                                                                 PRIOR APPLICATION NUMBER: 60/124,270
                                                                                                                                     TITLE OF INVENTION: Nucleic Acids, Proteins FILE REFERENCE: PA101
                                                                                                                                                              APPLICANT: Craig Rosen, APPLICANT: Steve Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
NAME/KEY: SITE
LOCATION: (68)
OTHER INFORMATION:
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SOFTWARE: PatentIn Ver. 2.0
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CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 81
TYPE: PRT
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                                                                                                                                                           Steve Ruben
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0020147140A1
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Pred. No. 1
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CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 329
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 56
LENGTH: 85
TYPE: PAT
ORGANISM: Homo sapiens
US-09-893-737-56
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US-10-108-605-281
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                                     ; ORGANISM: Drosophila melanogaster US-10-108-605-281
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APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41
                                                                                          SOFTWARE: Patentin Ver.
SEQ ID NO 281
LENGTH: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 281, Application US/10108605 Patent No. US20020160934A1
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Best Local (
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 Query Match
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                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                  APPLICANT: Broadus, Julie
APPLICANT: Stam, Lyn
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133B
                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/761,142 PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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NAME/KEY: SITE
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Local Similarity 100.0%;
hes 4; Conservative 0
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60 SLDA 63
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thes 0;
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US-09-931-071-11
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APPLICANT: Bertin, John
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-335001
CURRENT APPLICATION NUMBER: US/09/931,071
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/428,252
PRIOR FILING DATE: 1999-10-27
                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09841879B
Patent No. US20020142979A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES
FILE REFERENCE: 07334-330001
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Matches
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11
LENGTH: 89
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                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/841,879B CURRENT FILING DATE: 2001-04-24 PRIOR APPLICATION NUMBER: US 09/728,721 PRIOR FILING DATE: 2000-12-01 PRIOR APPLICATION NUMBER: US 09/340,620 PRIOR FILING DATE: 1999-06-28
                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                  LENGTH: 90
                 1 SLDA 4
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25 SLDA 28
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                                                                  Conservative
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Pred. No.
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RESULT 34 US-10-002-974-21 ; Sequence 21, Ap

Application US/10002974

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APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Ogur, Yasumori
TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
FILE REFERENCE: UM-06645
CURRENT APPLICATION NUMBER: US/10/014,269
CURRENT FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
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US-10-014-269-21
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: LENGTH: 92

: TYPE: PRT

: ORGANISM: Homo sapiens

US-10-002-974-21
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Best Local S
Matches 4
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APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1e1 Polynucleotides from Atherogenic Cells :
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
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TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
FILE REFERENCE: UM-06646
CURRENT APPLICATION NUMBER: US/10/002,974
CURRENT FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 99
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Local Similarity 100.0%;
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Cho, Judy
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Pred. No. 1
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Pred. No. 1
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1.7e+02;
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RESULT 38
US-09-905-243-49
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LOCATION: (50)...(66)
COTHER INFORMATION: CDRII
US-09-905-243-48
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US-09-905-243-48
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Sequence 49, Application US/09905243
Patent No. US20020062009A1
GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
TITLE OF INVENTION: Immunogenicity
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H
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SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 48
LENGTH: 98
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Patent No. US20020062009A1
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LENCTH: 96
TYPE: PRT |
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Best Local Similarity
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CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Monoclonal Antibodies with Reduced TITLE OF INVENTION: Immunogenicity FILE REFERENCE: P50770
                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: DOMAIN
LOCATION: (31)...(35)
OTHER INFORMATION: CDRI
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PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Macaca cynomolgus
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18;
Pred No.
                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                               9e+02;
                                                                                                                                                                                                                                                                                                                                            Length 98;
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                                                                                                                                                                                                                                                                                                           0;
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US-09-939-980-515; Sequence 515, A
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NUMBER OF SEQ ID NOS: 97
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 49
LENGTH: 98
TYPE: PRT
ORGANISM: Macaca cynomolgus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. US20020082234A1 GENERAL INFORMATION:
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LOCATION: (50)...(66)
OTHER INFORMATION: CDRII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: DOMAIN
LOCATION: (31)...(35)
OTHER INFORMATION: CDRI
                TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ward, Judith
TITLE OF INVENTION: No. US20020082234A1el Prokaryotic Polynucleotides,
NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS:
                                                                                                                                                      APPLICATION NUMBER: 08/936,165
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,980
FILING DATE: 27-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                    REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 510-270-4478
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                        NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                   TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burnham, Martin
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Pred. No. 1.9e+02;
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TOPOLOGY: linear
; MOLECULE TYPE: Protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 515:
US-09-939-980-515
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SOFTWARE: Fa.
SEQ ID NO 231
LENGTH: 109
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APPLICANT: Bertin, John
                                                                                                                                                                                                                                                                                                                        Sequence 231, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Appropriate Publication No.
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Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR ETILING DATE: 199-02-05
PRIOR ETILING DATE: EARLIER FILLING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR ETILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILLING DATE: 1998-06-17
PRIOR FILLING DATE: EARLIER FILLING DATE: 1998-02-06
PRIOR: FILLING DATE: EARLIER FILLING DATE: 1998-02-06
                                                                               PRIOR APPLICATION NUMBER: US 09/199,637
PRIOR ETLING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: US 60/066,517
PRIOR FILING DATE: 1997-11-25
                                                                                                                                                     FILE REFERENCE: 00786/361003
CURRENT APPLICATION NUMBER: US/09/975,719
CURRENT FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEXEOF
FILE REFERENCE: 0734/11801
CURRENT APPLICATION NUMBER: US/10/118,984
CURRENT FILING DATE: 2002-04-09
                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                        TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                             APPLICANT: Ausubel, Frederick M. APPLICANT: Rahme, Laurence G.
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 109
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    109
                                           FastSEQ for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
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                                           Windows Version 4.0
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Pred. No. 2e+02;
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US-10-105-931-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/340,620
PRIOR FILING DATE: 1999-06-28
PRIOR PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-728-721-6
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                          Query Match
Best Local S
                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10105931
Patent No. US20020150987A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
                                                                               LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
-10-105-931-6
           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/105,931
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR FILING DATE: 1998-02-06
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                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: 07334-076001
                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-124001
CURRENT APPLICATION NUMBER: US/09/728,721
CURRENT FILING DATE: 2000-12-01
CURRENT FILING DATE: 2000-12-01
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       Similarity 4; Conserv
     Conservative
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100.0%; Score 18; DB 12; 100.0%; Pred. No. 2.1e+02; O. Mismatches 0;
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Pred. No. 2.1e+02;
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Pred. No. 2.1e+02;
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                                    Length 109;
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Gaps
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                                                                                                                          Query Match
Best Local Similarity
"hes 4; Conservations
Search completed: February Job time: 6.83333 secs
                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-867-550-1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 45
US-09-867-550-1788
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; TYPE: PAT
; ORGANISM: Toxoplasma gondii
US-09-216-393-58
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US-09-216-393-58
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1788
LENGTH: 118
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Leach,
APPLICANT: Mehrab
APPLICANT: Conley
APPLICANT: Law, D
APPLICANT: Topper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1788, Application US/09867550 Patent No. US20020082206A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 08/994,825
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 58, Application US/09216393
PATENT NO. US/2010014447A1
GEMERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: TX-1-C2
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206 | Polynucleotides from Atherogenic Cells a
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313) |
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208/427
PRIOR APPLICATION NUMBER: USSN 60/208/427
PRIOR FILING DATE: 2000-05-30
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Best Local Similarity 100.0%;
                                                                       110 SLDA 113
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Conley, Pamela
                                                                                                                                           100.0%; Score 18; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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Pred. No. 2.3e+02;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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19.366 Million cell updates/sec
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:/cgn2_6/ptodata/1/paa/US09_COMB.pep:*
:/cgn2_6/ptodata/1/paa/US09_COMB.pep:*
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PCT-US94-11416-48
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Sequence 45, Appl
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e 15, 65, P	Sequence 15, Appl	- 1 ⊢	. Ф	96	32,	32,	Sequence 96, Appl	96,	Sequence 32, Appl	,	9,0	'nω	2, 7	e L	l3, Ag	Sequence 647, App	271,	12,	25,	Sequence 12, Appl	e 12,		Sequence 10, Appl	44		- + - +	44,	41,	44,	equence 41,	e 53,	equence 53,	equence 5	53. An

ALIGNMENTS

. Query Match	US-08-981-824-45	; ORGANISM: Homo sapiens	; TYPE: PRT	; LENGTH: 6	; SEQ ID NO 45	; SOFTWARE: PatentIn Ver. 2.1	; NUMBER OF SEQ ID NOS: 47	; EARLIER FILING DATE: 1995-07-14	; EARLIER APPLICATION	; EARLIER FILING DATE: 1996-07-15	; EARLIER APPLICATION	; CURRENT FILING DATE: 1998-09-18	; CURRENT APPLICATION	; FILE REFERENCE: 564-7029	; TITLE OF INVENTION	; TITLE OF INVENTION	; APPLICANT: JUNG, Gunther-Gerhard	; APPLICANT: VAN EN	; APPLICANT: BOITAR	; APPLICANT: SCHENDI	; APPLICANT: ALBERT	; APPLICANT: STAHL, Peter	; APPLICANT: ENDL, Josef	; GENERAL INFORMATION:	; Sequence 45, Application US/08981824	US-08-981-824-45	RESULT 1
100.0%; Score 18;	•	piens				1 Ver. 2.1	NOS: 47	TE: 1995-07-14	EARLIER APPLICATION NUMBER: DE/195 25 784.7	TE: 1996-07-15	EARLIER APPLICATION NUMBER: PCT/EP96/03093	TE: 1998-09-18	CURRENT APPLICATION NUMBER: US/08/981,824	54-7029	TITLE OF INVENTION: DECARBOXYLASE (GAD)	TITLE OF INVENTION: AUTOREACTIVE PEPTIDES FROM HUMAN GLUTAMIC ACID	Sunther-Gerhard	VAN ENDERT, Peter	BOITARD, Christian	SCHENDEL, Dolores	ALBERT, Winfried	Peter	Josef	Ζ.:	cation US/08981824		
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DB 13;																MUH MC											
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RESULT 3
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                                                                                                                               Sequence 48, Application US/08462860 GENERAL INFORMATION:
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino ***
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GENERAL INFORMATION:
APPLICANT: The University of Penns
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/136
FILING DATE: 14 October 19
ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
                                              APPLICANT: Barry S. Cooperman, Harvey Rubin,
APPLICANT: Jerome Salem, and Alison L. Fisher
TITLE OF INVENTION: "Peptide Inhibitors of
TITLE OF INVENTION: plasmodium Falciparum Ribonucleotide Reductase"
NUMBER OF SEQUENCES: 67
                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               REGEAUTION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 39:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEPAX: (215) 568-5549
TELEPAX: (215) 568-5549
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US
FILING DATE: Not Yet Assi:
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MEDIUM TYPE: Diskette,
   STREET:
CITY: F
                            ADDRESSEE:
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Philadelphia
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Suite 1800, Two Penn Center Plaza
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US-08-462-860A-48
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Best Local :
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cooperman, Barry S.
APPLICANT: Rubin, Harvey
APPLICANT: Salem, Jerome
APPLICANT: Fisher, Alison L.
TITLE OF INVENTION: RIBONUCLEO
TITLE OF INVENTION: REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: None INFORMATION FOR SEQ ID NO:
                             FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136,743
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
FILING DATE: 14-OCT-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 391
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEPAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/136,743
FILING DATE: 0ctober 14, 1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                      ZIP:
                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                     CITY: Philadelphia
                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1
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19102-1786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 amino acids
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                   14-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                      REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                    RIBONUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 18; DB 8; 100.0%; Pred. No. 4.2e+06;
                                                                                                                                                                                                                                                                                  GONDA, LAVORGNA & MONACO, P.C., Two Penn Center Plaza
                                                                                                                                                                                                                                                                                                                                       69
                                                                                                 US/08/462,860A
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US-09-194-218-44
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; MOLECULE TYPE: peptide
US-08-462-860A-48
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US-09-194-218-41
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Best Local
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            TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF FILE REFERENCE: 016786/0214

CURRENT APPLICATION NUMBER: US/09/194,218

CURRENT FILING DATE: 1999-02-05

EARLIER APPLICATION NUMBER: PCT/AU97/00312

EARLIER FILING DATE: 1997-05-22

EARLIER APPLICATION NUMBER: AU PN9990

EARLIER APPLICATION NUMBER: AU PN9990

EARLIER FILING DATE: 1996-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, NORMAN L.
APPLICANT: WESTBROOK, Simon L.
APPLICANT: WESTBROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
FILE REFERENCE: 016786/0214
CURRENT FILLING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: W5/09/194,218
EARLIER APPLICATION NUMBER: PCT/AU97/00312
EARLIER FILLING DATE: 1997-05-22
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                                                                                                                                                                                         APPLICANT: KINGSTON, David J. APPLICANT: GERRATY, Norman L. APPLICANT: WESTBROOK, Simon L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.0
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REFERENCE/DOCKET NUMBER: 39
TELECOMMUNICATION INFORMATION:
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Local Similarity 100.0%;
les 4; Conservative 0
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STRANDEDNESS:
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SEQ ID
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Pred. No. 4
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s 0;
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                                                                                                    US-09-396-347D-53
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                                                                                                               SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 53
LENGTH: 7
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/396,347B
CURRENT EILING DATE: 1999-09-14
PRIOR APPLICATION NUMBER: 09/001,984
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 53, Application US/09396347B GENERAL INFORMATION:
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                                          Matches
                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                     CURRENT FILING DATE: 1999-09-14
PRIOR APPLICATION NUMBER: 09/001,984
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                            APPLICANT: Laal, Suman APPLICANT: Zolla-Pazner, Sus APPLICANT: Belisle, John T TITLE OF INVENTION: EARLY DET FILE REFERENCE: 32004-169276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Belisle, John T
TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
FILE REFERENCE: NYU-11/CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Laal, Suman
APPLICANT: Zolla-Pazn
APPLICANT: Belisle, J
                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/396,347D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 7
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mycobacterium tuberculosis strain H37Rv
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                                       Score 18; DB 1/,
Pred. No. 4.2e+06;
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Pred. No. 4.2e+06;
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Pred. No. 4.2e+06;
Mismatches 0;
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RESULT 11
US-09-758-128-41
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US-09-396-347F-53
Sequence 41, Application US/09758128
GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, Norman L.
APPLICANT: WESTBROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
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SEQ ID NO 53
LENGTH: 7
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Best Local Similarity
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PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zolia-Pazner, Susan
APPLICANT: Belisle, John T
TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
FILE REFERENCE: 32004-169276
CURRENT APPLICATION NUMBER: US/09/396,347F
CURRENT FILING DATE: 1999-09-14
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APPLICANT: Zolla-Pazne
APPLICANT: Belisle, Jo
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CURRENT APPLICATION NUMBER: US/09/396,347E
CURRENT FILING DATE: 1999-09-14
PRIOR APPLICATION NUMBER: 09/001,984
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zolla-Pazner, Susan
APPLICANT: Belisle, John T
TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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les 4; Conservative
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Pred. No. 4.2e+06;
; Mismatches 0;
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RESULT 13
US-09-758-198-41
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US-09-758-128-44
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Best Local
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CURRENT APPLICATION NUMBER: US/09/758/198

CURRENT FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US/09/194,218

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312

PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
                                                                                                                                                    APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, Norman L.
APPLICANT: WESTBROOK, Simon L.
APPLICANT: WESTBROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
FILE REFERENCE: 016786/0214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/758,128
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
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APPLICANT: GERRATY, NORMAN L.
APPLICANT: WESTBROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
FILE REFERENCE: 016786/0214
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Best Local
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PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
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CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
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NUMBER OF SEQ ID NOS: 58
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Similarity 100.0%;
4; Conservative (
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Pred. No. 4.2e+06;
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Pred. No.
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TITLE OF INVENTION: WODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: WODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
FILE REFERENCE: 016786/0214
CURRENT APPLICATION NUMBER: US/09/758,198
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PAtentin Ver. 2.0
SEQ ID NO 44
LENGTH: 7
TYPE: PRT
ORGANITY
Sequence 41. Application US/09758426

GENERAL INFORMATION:

APPLICANT: KINGSTON, David J.

APPLICANT: GERRATY, NORMAN L.

APPLICANT: WESTBROOK, Simon L.

TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND US FILE REFERENCE: 016786/0214

CURRENT APPLICATION NUMBER: US/09/758,426

CURRENT FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: 09/194,218

PRIOR APPLICATION NUMBER: 09/194,218

PRIOR APPLICATION NUMBER: 09/194,218

PRIOR APPLICATION NUMBER: 09/194,218

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 58

SOFTWARE: Patentin Ver. 2.0

LENGTH: 7
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US-09-758-198-44
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US-09-758-426-41
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US-09-758-198-44
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NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 4.2e+06;
tive 0; Mismatches 0;
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US-09-861-661-41
; Sequence 41, Application US/09861661
; GENERAL INFORMATION:
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Best Local Similarity
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; ORGANISM: Rat
US-09-758-426-44
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Query Match
Best Local Similarity 100.
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SEQ ID NO 44
LENGTH: 7
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GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, NORMAN L.
APPLICANT: WESTBROOK, Simon L.
APPLICANT: WESTBROOK, Simon L.
APPLICANT: WESTBROOK, Simon L.
APPLICANT: WESTBROOK, Simon L.
APPLICANT: WESTBROOK, SAMON L.
TITLE OF INVENTION: — PEPTIDES, ANTIBODIES, VACCINES OR THEIR RECEPTORS
TITLE OF INVENTION: — PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
EILE REFERENCE: 016786/0214
CURRENT APPLICATION NUMBER: US/09/758,426
CURRENT FILING DATE: 1090-02-05
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR APPLICATION NUMBER: AU PN9990
DEBICOR ETITING PARS. 1006-05-1-20
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Matches 4; Conserv
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PRIOR FILING DATE: 1996-05-22
NUMBER OF SEO ID NOS: 59
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: GERRAFY, NORMAN L.
APPLICANT: WESTBROOK, SIMON L.
TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
FILE REFERENCE: 054270/0135
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NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2001-05-22
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/194,218 PRIOR FILING DATE: 1999-02-05
                                                                                                                                                                 LENGTH:
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                                            100.0%; Score 18; DB 22; 100.0%; Pred. No. 4.2e+06;
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Pred. No. 4.2e+06;
                            Mismatches
                                                             Length 7;
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US-09-997-900-10
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/09997900 GENERAL INFORMATION:
APPLICANT: Rakefuda, Genichi
APPLICANT: Costello, Colleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 44
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GENERAL INFORMATION:
APPLICANT: KINGSTON, DAVID J.
                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 10
      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sun, Ming
APPLICANT: Hu, Weining
TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
TITLE OF INVENTION: in Plants
FILE REFERENCE: 043753/241148 (5849-20A)
CURRENT APPLICATION NUMBER: US/09/997,900
CURRENT APPLICATION NUMBER: US/09/997,900
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/106,239
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/861,661
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: AU PN9990
PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GERRATY, NORMAN L.

APPLICANT: WESTBROOK, SIMON L.

TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
FILE REFERENCE: 054270/0135
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 11 SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/426,568 PRIOR FILING DATE: 1999-10-22
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                                                                                                                                                                NAME/KEY: PEPTIDE
LOCATION: (1)..(7)
OTHER INFORMATION: N-terminal sequence
OTHER INFORMATION: of plasmid F2
                                                                                                                                                                                                                                                                  LENGTH: 7
TYPE: PRT
ORGANISM: Arabidopsis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 7
TYPE: PRT
ORGANISM: Rattus sp.
                                                                                                        NAME/KEY: SITE LOCATION: (1)..(2) OTHER INFORMATION:
                                                                                                                                                                                                                                                                FEATURE:
                      Local
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  Similarity 4; Conserv
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100.0%; Score 18; DB 23; larity 100.0%; Pred. No. 4.2e+06; Conservative 0; Mismatches 0;
                                                                                                      Thrombin cleavage site
                                                                                                                                                                                           of AHAS small subunit peptide
                                          Length 7;
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Indels
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Gaps
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                                                                                                                                                                                                                                                                                                              RESULT 21
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                                                                                                                                                                                                                                                                                             US-08-813-273-12
                                                                                                                                                             Sequence 12, Application US/08813273
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Method of Identifying Molecules That
TITLE OF INVENTION: Home to a Selected Organ or Tissue In
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Applicat GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (619) 535-89-
TELEFAX: (619) 535-89-
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,708
FILING DATE: 11-SEP-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                    COMPUTER READABLE FORM:
                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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APPLICANT: Pasqualini, Rena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                         STATE:
                                                                                            CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100. ses 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 92122
                                       ZIP: 92122
                                                        COUNTRY:
                                                                                                           STREET:
                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                    California
C: United States
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: United States
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                                                                                                         E: Campbell & Flores LLP 4370 La Jolla Village Drive, Suite 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   both
Floppy disk
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Pred. NO. 4.2e+06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 8;
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OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

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US-09-228-866-12
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                                                                     CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,708
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-LJ 3430
REFERENCE/DOCKET NUMBER: P-LJ 3430
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9901
TELEPHONE: (619) 535-9901
TELEPHONE: (619) 535-9949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9049
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/09228866 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Molecules That Home to a Selected Organ
TITLE OF INVENTION: In Vivo
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TOPOLOGY: bo
MOLECULE TYPE:
-228-866-12
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GY: linear
                                                     amino acid
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                                       both
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RESULT 24
US-09-922-227-12
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US-09-700-993-25
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GENERAL INFORMATION:
APPLICANT: Rucelahti, Erkki
APPLICANT: Repalablini, Renata
TITLE OF INVENTION: Method of Identifying Molecules That
Home to a Selected Organ In Vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/700,993
CURRENT FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: JP98/141717
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
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Best Local Similarity 100
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KOBAYASHI, KAZUO APPLICANT: TAKEUCHI, MAKOTO
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TYPE: PRT
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                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/922,227
FILING DATE: 02-Aug-2001
CLASSIFICATION: <UNknown>
                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                    ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
           APPLICATION NUMBER: US 08/526,710 FILING DATE: 11-SEP-1995
                                                                                                                                                                                                                                                                         STATE: California
                                                                                                                                                                                                                                                      COUNTRY: United States
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IWAMATSU, AKIHIKO
YAMAMOTO, KENJI
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YOSHIDA, SATOSHI
APPLICATION NUMBER: US 08/813,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09700993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 18; DB 21; 100.0%; Pred. No. 4.2e+06;
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Pred. No. 4.2e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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RESULT 26
US-10-014-340-647
; Sequence 647, Application US/10014340
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: homo sapien US-09-988-493-271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 25
US-09-988-493-271
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MOLECULE TYPE: peptide;

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-922-227-12
                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 308
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 271, application US/09988493 GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/GB01/01219
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: GB 0006695.1
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: GB 0007265.2
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
APPLICANT: O'Hare, Michael John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/988,493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Waterfield, Michael Derek
TITLE OF INVENTION: Proteins, Genes, and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 2543-1-024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                          1 SLDA 4
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FILING DATE: 23-MAY-1997
APPLICATION NUMBER: US 09/227,906
FILING DATE: 08-JAN-1999
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
                                                                                                                                                                                                    SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page, Martin John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rajesh Bhikhu
                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                             Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18; DB 23;
Pred. No. 4.2e+06;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                           4.2e+06;
                                                                                                                                                                                                                                                                                                               DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breast Cancer
                                                                                                                                                                                                                                                                                                         Length 8;
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RESULT 28
US-09-109-836-13
Sequence 13, Application US/09109836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; SEQ ID NO 647
; LENGTH: 8
; TYPE: PRT
                                                                                                                                                                     Matches
                                                                                                                                                                  Best Local Similarity Matches 4; Conserv
                                                                                                                                                                                                Query Match
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APPLICANT: The General Hospital Coi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US97/21437
ETILING DATE: 26-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION UMBER: 60/031,607
FILING DATE: 27-NOV-1996
ATTOREY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/360WO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
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CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                   TELEX:
                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Fish & ALLEGE STRRET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                     1 SLDA 4
                                                                                                                                                                                                                                                                          CENGTH:
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                                                                                                       SLDA 10
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                                                                                                                                                                                                                                                                        10 amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette
                                                                                                                                                                                                                                                                          acids
                                                                                                                                                                               100.0%;
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                                                                                                                                                                  0;
                                                                                                                                                                 Score 18; DB Pred. No. 4.8 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                00786/360WO2
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                                                                                                                                                                                4.8e+02;
                                                                                                                                                                                            Length 10;
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                                                                                                                                                               Gaps
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RESULT 29
US-08-188-354-2
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                                                                                                                                                                                                                                                               Sequence 2, Application US/08188354
GENERAL INFORMATION:
APPLICANT: COMAN, Nicholas J.
TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF MAKING AND USING THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/109,83
ETILING DATE: 02-JUL-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/977,836
ETILING DATE: 26-NOV-1997
APPLICATION NUMBER: 60/031,607
ETILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS: LENGTH: 10 amino acids
              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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TELEFAX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jacobowitz Israel, Esther APPLICANT: Simister, Neil E.
                                                                                                                                                                            STREET: 419 Sever
                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   r Match 100.0%; Score 18; DB 15; Local Similarity 100.0%; Pred. No. 4.8e+02; es 4; Conservative 0; Mismatches 0:
                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fraser, Janis K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 225 |
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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02110-2804
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                                                                                                                                                                                                  419 Seventh Street, N.W., Suite 300
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                                                                                                                                                                                                                   BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette
28-JAN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                            US-08-461-383-96
                                                              RESULT 31
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US-09-831-253A-3
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             ; Sequence 96, Applicat; GENERAL INFORMATION:
                                                                                                                                                                       Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: EZQUERRO SAENZ, Ignacio Jose
APPLICANT: LASARTE SAGASTIBELZA, Juan Jose
APPLICANT: PRIETO VALTUENA, Jesus
APPLICANT: BORRAS CUESTA, Francisco
TITLE OF INVENTION: TGF(b1-inhibitor peptides
FILE REFERENCE: U013446-9
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 3
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/831,253A CURRENT FILING DATE: 2001-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 248633
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 11-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, G. Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0: FILING DATE: 11-JUN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ON NUMBER: US 07/897,162
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino a STRANDEDNESS:
                                                                                                                                                                       Local Similarity les 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/
FILING DATE: 11-JUN-1993
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                                                                                                                                        1 SLDA 4
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                                                                                                            SLDA
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                               Application US/08461383
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FOWLKES, Dana M.
                                                                                                                                                                         Conservative
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                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                     Score 18; DB 22;
Pred. No. 5.9e+02;
                                                                                                                                                                         Mismatches
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APPLICANT: APPLICANT:

BROACH, Jim MANFREDI, John KLEIN, Christine

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APPLICANT:

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                                                                                                                                                                             Sequence 96, Application US/08463181 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100. Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                             APPLICANT: APPLICANT:
                                TITLE OF INVENTION:
                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CPI-012CP4B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-227-7400
                NUMBER OF
                                                              APPLICANT:
                                                                               APPLICANT:
                                                                                                APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASIFICATION: 435
PRIOR APPLICATION DATA:
US 08/322,137
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TELEFAX: 752806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US OFFILING DATE: 31-JAN-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/309,313
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 01
FILING DATE: 13-OCT-1994
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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               SEQUENCES:
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PAUL, Jeremy
TRUEHEART, Joshua
VENTION: YEAST CELLS ENGINEERED TO PRODUCE
VENTION: PHERMONE SYSTEM PROTEIN SURROGATES,
EQUENCES: 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       617-227-5941
                                                                                                                                            BROACH, Jim
                                                                                            MURPHY, Andrew J.
                                                                                                             KLEIN, Christine
                                                                                                                         MANFREDI, John
                                                                                                                                                           FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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YEAST CEL
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Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                   Length 13;
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                       AND USES THEREFOR
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US-08-689-172A-32

; Sequence 32, Application US/08689172A

; GENERAL INFORMATION: Chaisting h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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PRIOR APPLICATION UNMBER: US 08/309,313
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/190,328
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/041 431
FILING DATE: 31-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 13 amino acids
                                                                                                                                                                               APPLICANT: Klein, CHARLES J. M. APPLICANT: Murphy, Andrew J. M. TITLE OF INVENTION: Methods and CTITLE OF INVENTION: Identifying
                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                       STREET: 60 St
CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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TELEFAX: 248633
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ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W!,
                                                                                                                                    ADDRESSEE: LAHIVE & COCKFIELD |
STREET: 60 State Street, suite 510
   OPERATING SYSTEM:
                     COMPUTER:
                                                                                     COUNTRY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                   5 SLDA
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                                                                     02109-1875
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                                                                                                       Massachusetts
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                                                                                       USA
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IBM PC compatible YSTEM: PC-DOS/MS-DOS
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IBM PC compatible
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Pred. No. 6.5e+02;
Mismatches 0;
                                                                                                                                                                                                        Receptor Effectors
                                                                                                                                                                                                                        Compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 13;
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                                                                           ; MOLECULE TYPE: US-08-689-172C-32
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NAME: KARA, Catherine J.
REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: CPI-012CP7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ. ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 32, Application US/08689172C
GENERAL INFORMATION:
APPLICANT: Klein, Christine A.
APPLICANT: Murphy, Andrew J. M.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Identifying Receptor Effectors
NUMBER OF SEQUENCES: 132
Query Match 100.0%; Score 18; I Best Local Similarity 100.0%; Pred. No. 6 Matches 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/689,172C
FILING DATE: 07-Aug-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: KARA, Catherine J.
REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: CPI-012CP7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                  TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
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CURRENT APPLICATION DATA:
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                                                                                                                                               LENGTH:
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                                                                                                                linear
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 Mismatches
                                      DB 10;
                   .5e+02;
                                  Length 13;
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밁
                                  δõ
                                                                                                                                                 ; MOLECULE TYPE: US-09-286-166-96
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                                                                       Matches
                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                           TELEPHONE: 617-227-7400
TELEFAX: 617-227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/461,383
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/322,137
FILING DATE: 13-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/461,383
APPLICATION NUMBER: 05 08/461,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: PAUL, Jeremy
APPLICANT: TRUEHEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR NUMBER OF SEQUENCES: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE AND COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CPI-012CP4B
                                                                                                                                                                                                                                                                                                                                                                        NAME: Vincent, Matthew P REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 31-MA
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CLASSIFICATION:
                                                                                                                                                                                      TOPOLOGY:
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                                  1 SLDA 4
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5 SLDA 8
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                                                                       Conservative
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                                                                                                                                                                  peptide
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20-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-1993
                                                                                     100.0%;
                                                                                                                                                                                                                                                            96:
                                                                       0;
                                                                     Score 18; DB 16;
Pred. No. 6.5e+02;
; Mismatches 0;
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Length 13; Indels

0,

Gaps

0;

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SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-309-196-96
                                                                                                   RESULT 37
US-09-747-774A-32
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                                                               Sequence 32, Application US/09747774A GENERAL INFORMATION:
                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,328
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVer P.
REGISTRATION NUMBER: E0LWKES=2C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                          APPLICANT: Klein, Christine A. APPLICANT: Murphy, Andrew J. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 96, Application US/09309196 GENERAL INFORMATION:
APPLICANT:
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
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APPLICANT: TRUEHEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                              1 SLDA 4
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: D.C.
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           Murphy, Andrew J. M. Broach, James R.
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KLEIN, Christine
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                                                                                                                                                                                                                                                           Score 18; DB 17;
Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                          Length 13;
                                                                                                                                                                                                                                          Indels
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RESULT 38
US-09-953-354-32
Sequence 32, Application US/09953354
GENERAL INFORMATION:
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; ORGANIEM: Saccharomyces cerevisiae
US-09-747-774A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 08/461,383
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/463,181
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/322,137
PRIOR FILING DATE: 1994-10-13
PRIOR FILING DATE: 1994-09-20
PRIOR FILING DATE: 1994-09-20
PRIOR APPLICATION NUMBER: US 08/399,313
PRIOR FILING DATE: 1994-09-20
PRIOR APPLICATION NUMBER: US 08/190,328
PRIOR APPLICATION NUMBER: US 08/041,431
PRIOR FILING DATE: 1993-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 98
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
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CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 08/582,333
PRIOR FILING DATE: 1996-01-17
PRIOR APPLICATION NUMBER: US 08/464,531
PRIOR FILING DATE: 1995-06-05
PRIOR PRIOR DATE: 1995-06-05
PRIOR FILING DATE: 1995-06-05
PRIOR FILING DATE: 1995-06-05
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TITLE OF INVENTION: Methods and Compositions for Identifying
TITLE OF INVENTION: Receptor Effectors
FILE REFERENCE: CPI-012CP5DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/689,172
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953,354
FILING DATE: 13-Sep-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Methods and Compositions for Identifying Receptor Effectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
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                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
                                                                                                                                                                                                                                                                                                                                 ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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Trueheart, Joshu
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RESULT 39
US-10-263-341-96
; Sequence 96, Application US/10263341
; GENERAL INFORMATION:
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Best Local :
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TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 32:
                 INFORMATION FOR SEQ ID NO: 96:
                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/322,137

FILING DATE: 13-OCT-1994

APPLICATION NUMBER: US 08/309,313

FILING DATE: 20-SEP-1994

APPLICATION NUMBER: US 08/190,328

FILING DATE: 31-JAN-1994

APPLICATION NUMBER: US 08/041,431

FILING DATE: 31-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 SLDA 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.,
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAUL, Jeremy
TRUEHEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
SEQUENCE
                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 119
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/263,341
FILING DATE: 01-Oct-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                            TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                  NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: CPI-012CP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                          TELEX:
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KLEIN, Christine
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                                        248633
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                                                                                                                             FOLWKES=2C
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TOPOLOGY: linear;

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-10-263-341-96
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OTHER INFORMATION: Description of Artificial Sequence: Derived from OTHER INFORMATION: the modified human type III receptor, position OTHER INFORMATION: 729-742
US-09-831-253A-6
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US-09-831-253A-6
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LENGTH: 14
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08400306 GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: PRIETO VALTUENA, Jesus APPLICANT: BORRAS CUESTA, Francisco TITLE OF INVENTION: TGF(b1-inhibitor FILE REFERENCE: U013446-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: EZQUERRO SAENZ, Ignacio
APPLICANT: LASARTE SAGASTIBELZA, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         APPLICANT: J.A. Kessler, A.J. Conley, B.A. Arnold
TITLE OF INVENTION: Selected Principal Neutralization
TITLE OF INVENTION: Epitopes for Antibody that Neutralizes HIV in Peripheral
TITLE OF INVENTION: Blood Mononouclear Cells
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
               APPLICATION NUMBER: FILING DATE:
                                                                                                                                               ZIP: 07065
                                                                                                                                                                             CITY: Rahway
STATE: NJ
                                                                                                                                                                                                            STREET:
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||||
5 SLDA 8
                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SLDA 4
CLASSIFICATION: 424
                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                              USA
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                                US/08/400,306
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Pred. No. 7e+02;
Mismatches
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Pred. No.
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RESULT 43
US-09-461-061-15
; Sequence 15, Application US/09461061
; GENERAL INFORMATION:
; APPLICANT: MCCTRE, Keith R.
; TITLE OF INVENTION: Inhibition of Angiogenesis By High Molecular Weight
; TITLE OF INVENTION: Kininogen Domain 3 Peptide Analogs
: FILE REFERENCE: 6056-260 US
: FILE TEPERENCE: 6056-260 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATI: Commonwealth System
in Title Of Invention: Inhibition of Angiogenesis By High Mol
intle Of Invention: Kininogen Domain 3 Peptide Analogs
intle Reference: 6056-260 pc
CURRENT APPLICATION NUMBER: PCT/US99/28465A
CURRENT FILING DATE: 1999-12-02
EARLIER APPLICATION NUMBER: 60/112,427
EARLIER APPLICATION NUMBER: 60/112,427
EARLIER APPLICATION NUMBER: 60/112,427
EARLIER FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
I SEQ ID NO 15
TYPE: PRT
ORGANISM: Artificial Commons
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meredith, Roy D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: 1907
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4678
TELEPAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SED ID NO: 1:
SECURACY CHARACTERISTS
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ANTI-SENSE: 1
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LENGTH: 15 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                        SLDA 11
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                                                                                                                                                                                                                                                                                                                       Conservative
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Pred. No.
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Pred. No. 7.6e+02;
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High Molecular Weight
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PCT-US02-09671-65; Sequence 65, Applica; GENERAL INFORMATION:
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; OTHER INFORMATION:
US-09-461-061A-15
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILLING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILLING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR FILLING DATE: 2001-10-01
PRIOR FILLING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/336,780
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FEARLIER APPLICATION NUMBER: 60/11
EARLIER FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 16
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LENGTH: 16
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GENERAL INFORMATION:
APPLICANT: McCrae, Keith R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US02/09671
CURRENT FILING DATE: 2002-03-28
                                                                                                                                                                                                  TITLE OF INVENTION: TRANSLATIONAL PROFILING FILE REFERENCE: 08191-026WO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Inhibition of Angiogenesis By High Molecular Weight TITLE OF INVENTION: Kininogen Domain, 3 Peptide Analogs

CURRENT APPLICATION NUMBER: US/09/461,061A

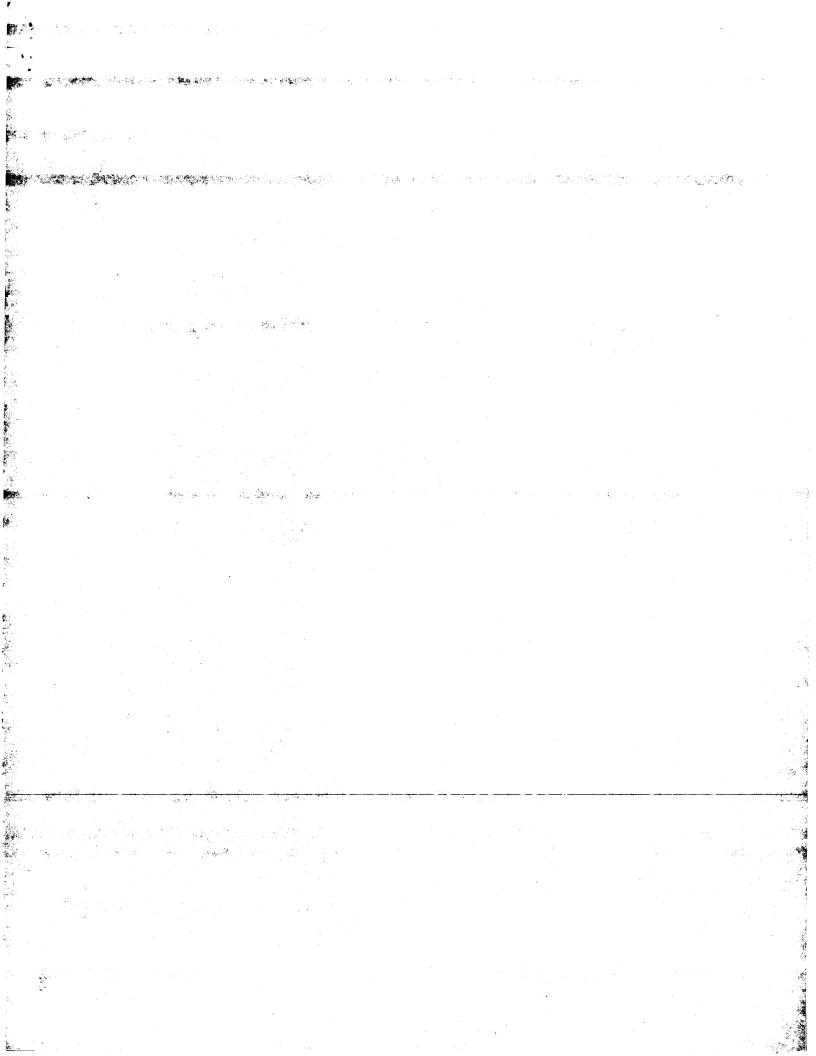
CURRENT FILING DATE: 1999-12-15

PRIOR APPLICATION NUMBER: 60/112,427 |
PRIOR APPLICATION NUMBER: 60/112,427 |
PRIOR APPLICATION NUMBER: 60/112,427 |
PRIOR FILING DATE: 1998-12-16

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                          APPLICANT: Zycos Inc.
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description of Artificial Sequence: Fragment of human HK domain \mathbf{3}^{\mathsf{T}}
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Pred. No.
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thes 0;
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8.2e+02;
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PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR PILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09671-65
Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1111
Db 7 SLDA 4
III
Db 7 SLDA 10
Search completed: February 6, 2003, 11:37:34
Job time: 134.167 secs
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Result
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PCT-US02-32727-17389
US-10-057-498-1738
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US-09-258-600-96 ·
; Sequence 96, Applicati
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION DATA:
APPLICATION UNMBER: US/99/258,600
FILING DATE: 26-Feb-1999
CLASSIFICATION: CUDKNOWN>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                    ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOLW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20004
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sequence 94, Appl sequence 8416, Ap sequence 8518, Ap sequence 8518, Ap sequence 2064, Ap sequence 2054, Ap sequence 6955, Ap sequence 6955, Ap sequence 28376, A sequence 11100, A sequence 13114, A sequence 27093, A sequence 210, App sequence 13114, Ap sequence 13114, Ap sequence 13114, Ap sequence 13114, Ap	21639, 7714,

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE PHEROMONE SYSTEM PROTEIN SURROGATE NUMBER OF SEQUENCES: 119 APPLICANT: FOWLKES, Dana M. BROACH, Jim STREET: 419 Seventh Street, Application US/09258600 MURPHY, Andrew J. PAUL, Jeremy KLEIN, Christine MANFREDI, John BROWDY AND NEIMARK

Seventh Street, N.W., PROTEIN SURROGATES, Suite AND USES THEREFOR

ALIGNMENTS

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati

Version #1.30

APPLICATION NUMBER: US/08/461,598
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/322,137
FILING DATE: 13-OCT-1994
APPLICATION NUMBER: US 08/309,313
FILING DATE: 20-SEP-1994
APPLICATION NUMBER: US 08/190,328
FILING DATE: 31-JAN-1994 APPLICATION NUMBER: US 08/041,431 FILING DATE: 31-MAR-1993

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RESULT 3
US-09-585-645A-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 25 May 2000 (25.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR PRIOR PRIOR OMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 31 SUPEMBER: US 09/608,408
PRIOR FILING DATE: 30 June 2000 (30.06.00)
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US-10-203-138A-12434
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                                                                                                                                                          Matches
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Molecular Dynamics Sequence Listing Engine SEQ ID NO 12434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12434, Application US/10203138A GENERAL INFORMATION:
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FILE REFERENCE: PD 0004 MO 8
CURRENT APPLICATION NUMBER: US/10/203,138A
CURRENT FILING DATE: 2002-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 15438
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 44
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Molecular Dynamics, Inc
                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: MAP TO AC005488.2
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                                                                            36 SLDA 39
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
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Rank, David R.
Hanzel, David K.
Chen, Wensheng
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                                                                                                                                                                                                                                                                                                                              EXPRESSED IN BT474, SIGNAL = 3.2
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                                                                                                                                                                    Score 18; DB 6;
Pred. No. 2.9e+02;
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                                                                                                                                                                                         Length 44;
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RESULT 5
US-10-057-498-24214
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; ORGANISM: Propioni acnes
PCT-US02-32727-24214
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SEQ ID NO 24214
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Best Local S
Matches 4
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Best Local Similarity
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SEQ ID NO 54
LENGTH: 45
TYPE: PRT
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
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PRIOR FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 70
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TITLE OF INVENTION: Compositions and Methods for Therapeutic
TITLE OF INVENTION: for Deafness, Osteoarthritis, and Abnorm
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                                                               5 SLDA
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Jones, Robert
Carter, Darrick
Barth, Brenda
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Bhatia, Ajay
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Hassan, Bessam
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; NAME/KEY: UNSURE
; LOCATION: 33
; OTHER INFORMATION: Xaa-His or Asn
US-09-513-999C-5438
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Matches
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SOFTWARE: Patent.pm
SEQ ID NO 5438
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LENGTH: 50
TYPE: PRT
ORGANISM: Propioni acnes
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APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION UNMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
                                                                             APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
APPLICANT: Bhatia, Ajay
APPLICANT: Maisonneuve, Jean
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CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
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                  APPLICANT
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                                             Wang,
                                                                             Persing, David
Bhatia, Ajay
Maisonneuve, Jean
Lodes, Michael
Benson, Darin
                                             Zhang, Yanni
Wang, Siqing
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Pred. No. 3.5e+02;
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; ORGANISM: Propioni acnes US-10-057-498-22975
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SEQ ID NO 22375
LENGTH: 53
TYPE: PRT
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LENGTH: 53
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Best Local Similarity
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             APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NITHIAND
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CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514
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CURRENT FILING DATE: 2002-
NUMBER OF SEQ ID NOS: 30992
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TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
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APPLICATION NUMBER: PCT/US02/32727 FILING DATE: 2002-10-11
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Carter, Darrick
Barth, Brenda
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Bhatia, Ajay
                                                                           Carter, Darrick
Barth, Brenda
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Wang, Siqing
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Persing, David
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Jones, Robert
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Pred. No. 3
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Pred. No. 3.5e+02
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3.5e+02;
                                          for the Therapy and Diagnosis of
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APPLICANT: Hanzel, David K.

APPLICANY: Chen, Wensheng

ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474

FILLE REFERENCE: PB 0004 WO 8

CURRENT FILING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 20 4 FEbruary 2000 (04.02.00)

PRIOR FILING DATE: 04 FEBRUARY DATE: 05.00)

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 03 OCTOBER 2000 (03.10.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR APPLICATION NUMBER: US 
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US-10-203-138A-11775
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US-10-057-498-17389
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; ORGANISM: Propioni acnes
PCT-US02-32727-17389
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Matches
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CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 17389
LENGTH: 54
TYPE: PRT
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APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
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Best Local Similarity
Matches 4; Conserv
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Molecular Dynamics Sequence Listing Engine
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Rank, David R.
Hanzel, David K.
                                            ID NOS:
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Pred. No. 3.6e+02;
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PCT-US02-32727-27113; Sequence 27113, Application PC/TUS0232727; GENERAL INFORMATION:
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                                                                                                                                                    RESULT 13
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                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
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SEQ ID NO 2538
LENGTH: 56
TYPE: PRT
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                                                     APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
APPLICANT: Bhatia, Ajay
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Best Local
                         APPLICANT:
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LENGTH: 55
                                         APPLICANT:
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CURRENT FILING DATE: 2002-10-11
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APPLICANT:
APPLICANT:
 APPLICANT:
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TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL =
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           Zhang, Yanni
Wang, Siqing
                                                  Persing, David
Bhatia, Ajay
Jen, Shyian
                                      Maisonneuve, Jean
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Jen, Shyian
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Bhatia, Ajay
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                                      Francois
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Pred. No.
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CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 27113
LENGTH: 56
TYPE: PRT
ORGANISM: Propioni acnes
US-10-057-498-27113
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CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 2538
LENGTH: 56
TYPE: PRT
RORANISM: Propioni acnes
US-10-057-498-2538
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CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 27113
LENGTH: 56
TYPE: PRT
ORGANIAM: Propioni acnes
PCT-US02-32727-27113
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Best Local Similarity
Query Match
Best Local Similarity
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                                                                                                                                                                                               JENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Vasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
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APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 18; DB 6; llarity 100.0%; Pred. No. 3.8e+02; Conservative 0; Mismatches 0;
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 100.0%;
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Pred. No. 3.8e+02;
 Score
Pred.
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18;
No.
 DB 6;
3.8e+02;
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PCT-US02-32727-27575
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             NUMBER OF SEQ ID NOS:
SEQ ID NO 27575
LENGTH: 57
TYPE: PRT
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Best Local Similarity
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LENGTH: 57
                                                                                                                                                                                                                                                                                                                                              Sequence 27575,
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                                                       APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
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  ORGANISM:
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Jen, Shyian
Lodes, Michael
Propioni acnes
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Jones, Robert
Carter, Darrick
Barth, Brenda
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Jen, Shyian
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Zhang, Yanni
Wang, Siqing
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Bhatia, Ajay
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Barth, Brenda
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Jones, Robert
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Wang, Siging
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Bhatia, Ajay
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Pred. No. 3.8e+02,
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; NAME/KEY: unsure
; LOCATION: (3)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-057-498-27575
RESULT 20
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US-10-057-498-27575
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; LOCATION: (3)
; OTHER INFORMATION: Xaa = Any Amino Acid
PCT-US02-32727-27575
                                                                                                                                                                                                                                            APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of FILE REFERENCE: 2101/21.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 27575
LENGTH: 57
TYPE: PRT
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Best Local S
Matches 4
                                                                                                   Matches
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Best Local :
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APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 23045
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27575,
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Best Local (
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                                         54 SLDA 57
                                                                                                   Local Similarity les 4; Conserv
                                                           1 SLDA 4
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Similarity 100.0%;
4; Conservative (
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                                                                                                            100.0%; Score 18; DB 6; 100.0%; Pred. No. 3.8e+02;
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Pred. No.
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Pred. No.
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; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 28196
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-USO2-32727-28196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 20121.514C1
CURRENT FILING BATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
TYPE: PRT
ORGANT: D. D. D. C. Compositions and Methods for the Therapy and Diagnosis of ...
CURRENT APPLICATION NUMBER: PCT/US02/32727
NUMBER OF SEQ ID NOS: 30992
TYPE: PRT
ORGANT: PCT/US02/32727
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                                                   Matches
                                                              Query Match
Best Local
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Best Local :
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CURRENT FILING DATE: 2002-10-11
NUMBER OF SEO ID NOS: 30992
                                                                                                                                                                                                APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121...14C1
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                                                              Local Similarity
28 SLDA
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                         1 SLDA 4
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Ten, Shyian
Micha
31
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Barth, Brenda
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Jones, Robert
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Bhatia, Ajay
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Jen, Shyian
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Wang, Siqing
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Bhatia, Ajay
                                                  Conservative
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                                                             Pred.
                                                          Score 18; DB 1;
Pred. No. 4e+02;
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Pred
                                               Mismatches
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RESULT 24
US-10-057-498-28196
; Sequence 28196, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
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; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 28948
; LENGTH: 59
; TYPE: PRT
; ORGANISM: P. Acnes
PCT-US02-32727-28948
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CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 16333
LENGTH: 59
TYPE: PRT
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                        28 SLDA 31
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les 4; Conserv
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Skeiky,
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Bhatia, Ajay
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Pred. No.
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Pred. No.
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US-10-057-498-28948
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APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnifile Reference: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 28948
ELENCTH: 59
TYPE: PRT
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Best Local Similarity
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LENGTH: 59
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Best Local
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CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 21639
LENGTH: 61
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TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
                                                                           APPLICANT: Jones, Robert
APPLICANT: Carter, Darrick
APPLICANT: Barth, Brenda
APPLICANT: Boughass, John
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
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Jen, Shyian
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Bhatia, Ajay
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Persing, David
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                                                                                                                                                                                                                                                       Jean
                                                                                                                                                                                                                                                      Francois
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); Mismatches
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Pred. No.
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Sequence 7714, Application US/09513999C
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dumas Miline Edwards, J.B.
APPLICANT: Dumas Miline Edwards, J.B.
APPLICANT: Dumas Miline Edwards, J.B.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7714
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                                                                                                                       ; OTHER INFORMATION: Xaa= *
US/09/513,999C-7714
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US-10-057-498-21639
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                                                             Matches
                                                                                        Query Match
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SEQ ID NO 21639
LENGTH: 61
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Matches 4; Conserv
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Best Local
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APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
                                                                                                                                                                                           LENGTH: 62
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mitcham, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Propioni acnes
                                                                                                                                                    NAME/KEY: UNSURE
LOCATION: 55
                                                                                                                                                                                      FEATURE:
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ORGANISM: Propioni acnes
 59
                                                                          Local Similarity
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                              1 SLDA 4
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SLDA 62
                                                           Conservative
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                                                     Score 18; DB 5; L
Pred. No. 4.2e+02;
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Pred. No.
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Pred. No. 4.2e+02;
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thes 0;
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                                                                                  Length 62;
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RESULT 30
US-10-301-997-94
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PCT-US02-32727-6416
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LENGTH: 63
TYPE: PRT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121,514C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mitcham, Jennifer APPLICANT: Skeiky, Yasir
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NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 28341/33996
TELECOMMUNICATION INFORMATION: |
TELEPHONE: (312) 474-6300
                                                                                     APPLICATION NUMBER: US/09/527,431
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US/08/887,534
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Holden, David W.
TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                APPLICATION NUMBER: US/10/301,997
FILING DATE: 22-NOV-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicago
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Jen, Shyian
Lodes, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Marshall, O'Toole,
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Jones, Robert
Carter, Darrick
Barth, Brenda
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Bhatia, Ajay
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30992
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RESULT 31
US-10-057-498-6416
; Sequence 6416, Application US/10057498
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Best Local S
Matches 4
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APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Vasir
APPLICANT: Skeiky, Vasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 6416
LENGTH: 63
TYPE: PRT
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NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 8518
LENGTH: 65
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                                          APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
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APPLICANT:
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INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
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mes 4; Conserv
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Skeiky, Yasir
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Ten, Shyian
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                                                                                                                       Carter, Darrick
Barth, Brenda
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Jones, Robert
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Bhatia, Ajay
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Pred. No. 4.3
0; Mismatches
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Pred. No. 4.3e+02;
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                                                                                          the Therapy and Diagnosis of Acnes
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RESULT 33
US-10-057-498-8518
Sequence 8518, Application US/10057498
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Vasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 8518
LENGTH: 65
TYPE: PRT
ORGANISM: Propioni acnes
US-10-057-498-8518
                                                        ; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 2064
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-USO2-32727-2064
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Best Local Similarity
Matches
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Best Local Similarity
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                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
                                                                                                                                                                        APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of
FILE REFERENCE: 210121.514C1
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Benson, Darin
Jones, Robert
Carter, Darrick
Barth, Brenda
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Jen, Shyian
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Bhatia, Ajay
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Conservative
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            Score 18; DB 1;
Pred. No. 4.7e+02;
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Pred. No. 4.5e+02;
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Pred. No. 4.5e+02;
Mismatches
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RESULT 37
PCT-US02-32727-28376
FCT-US02-32727-28376
FCT-US02-32727-28376
FCT-US02-32727-27
FCENERAL INFORMATION:
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PCT-US02-32727-6955
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US-10-057-498-2064
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CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 6955
LENCTH: 70
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
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APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 2064
LENGTH: 68
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TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
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Barth, Brenda
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Jones, Robert
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                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 18; DB 1; 100.0%; Pred. No. 4.8e+02; No. 4.
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Pred. No. 4.7
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for the Therapy and Diagnosis of Acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 70;
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RESULT 39
US-10-057-498-28376
US-10-057-498-28376, Application US/10057498
GENERAL INFORMATION:
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US-10-057-498-6955
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NAME/KBY: unsure
LOCATION: (40)
OTHER INFORMATION: Xaa =
PCT-US02-32727-28376
                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 6955
LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6955, Application US/10057498 GENERAL INFORMATION:
                       APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 28376
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 29212
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TYPE: PRT
ORGANISM: Propioni
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Skeiky, Yasir
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Barth, Brenda
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Jones, Robert
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Jen, Shyian
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Wang, Siqing
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Bhatia, Ajay
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Pred. No. 4.8e+02;
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Pred. No. 4.8e+02;
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PRIOR FILING DATE: 04 February 2000 (94.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR FILING DATE: 21 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/508,408
PRIOR FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 15438
SOFTWARE: Molecular Dynamics Sequence Listing Engine SEQ ID NO 11100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; NAME/KEY: unsure
; LOCATION: (40)
; OTHER INFORMATION: Xaa - Any Amino Acid
US-10-057-498-28376
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CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 28376
LENGTH: 70
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative (
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                                                                   Matches
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FILE REFERENCE: PB 0004 W0 8
CURRENT APPLICATION NUMBER: US/10/203,138A
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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24 SLDA 27
1 SLDA 4
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                                                                                         ocal Similarity
                                                              100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                    SWISSPROT HIT: Q15750, EVALUE 4.00e-36
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Pred. No. 4.8
D; Mismatches
                                                                Score 18; DB 6;
Pred. No. 4.8e+02;
); Mismatches 0;
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thes 0;
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                                                                 ; ORGANISM: Propioni acnes PCT-US02-32727-27093
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Best Local S
Matches 4
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LENGTH: 72
TYPE: PRT
                                                                                                             SEQ ID NO 27093
LENGTH: 72
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                Query Match
Best Local
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APPLICANT: Barth, Brenda
APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
                                                                                                                                                                                                                                                                                           APPLICANT: APPLICANT:
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CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514C1
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 Similarity 4; Conserv
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Barth, Brenda
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Lodes, Michael
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Jones, Robert
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Wang, Siqing
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Bhatia, Ajay
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Jones, Robert
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Bhatia, Ajay
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100.0%;
ilarity 100.0%;
Conservative 0
 Score 18; DB 1;
Pred. No. 5e+02;
Mismatches
                                 DB 1;
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                                                                                                                                                                                                            for the Therapy and Diagnosis of Acne
                               Length 72;
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   Indels
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   Gaps
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SLDA 4

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RESULT 45
US-10-057-498-27093
; Sequence 27093, Application US/10057498
; GEMERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 44
US-10-057-498-13114, Application US/10057498
; Sequence 13114, Application US/10057498
; GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-13114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 210
LENGTH: 72
TYPE: PRT
ORGANISM: Lactobacillus rhamnosus
US-10-264-213-210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 43
US-10-264-213-210
; Sequence 210, Applica
; GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity 100
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Havukkala, Ilka J
APPLICANT: Lubbers, Mark William
APPLICANT: Dekker, James
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: them, and methods for using them.
FILE REFERENCE: 11000.1043c3
CURRENT APPLICATION NUMBER: US/10/264,213
CURRENT FILING DATE: 2002-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Glenn, Matthew
                                                                                                                                                                                                                                           66 SLDA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 SLDA 17
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Pred. No.
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                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-27093
Search completed: February
Job time : 15 secs
                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                       CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 27093
LENGTH: 72
                                                     66 SLDA 69
                                                                              1 SLDA 4
                                                                                                           Conservative
                                                                                                                     100.0%;
           6, 2003, 11:39:03
                                                                                                           0,
                                                                                                                     Score 18; DB 6; Length 72; Pred! No. 5e+02;
                                                                                                        Mismatches
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Gaps

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein -
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                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein search, using
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Match
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                Length
   DB
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  HPRB
H1539
A81539
G83935
A69435
ZGBPT9
E841679
E84179
H97373
AB2591
T44780
T09293
T199285
T19931
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H70537
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AC2450
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A72031
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G86126
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                               DNA-binding protei embryonic abundant
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Query Match 100.0%; Best Local Similarity 100.0%; Matches 4: Conservative	RESULT 2 G86126 hypothetical protein 25889 [imported] - E C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16 C;Date: 16-Feb-2001 #sequence_revision 16 C;Accession: G86126 R;Perna, N.T.; Plunkett III, G.; Burland, iller, L.; Grotbeck, E.J.; Davis, N.W.; L Nature 409, 529-533, 2001 A;Title: Genome sequence of enterchemorrh A;Reference number: A85480; MUID:21074935 A;Accession: G86126 A;Accession: G86126 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-33 <sto> A;Cross-references: GB.AE005174; NID:g125 A;Experimental source: strain 0157:H7, su C;Genetics: A;Gene: Z5889</sto>	Query Match 100.0%; Best Local Similarity 100.0%; Matches 4; Conservative Qy 1 SLDA 4 LIII Db 12 SLDA 15	RESULT 1 A44921 A44921 hydroxypyruvate reductase (EC 1.1.1.81) - Methylobacterium extorquens C;Species: Methylobacterium extorquens C;Species: O1-Apr-1993 #sequence_revision 18-Nov-1994 #text_chai C;Accession: A44921 R;Chistoserdova, L.V.; Lidstrom, M.E. J Bacteriol. 174, 71-77, 1992 A;Title: Cloning, mutagenesis, and physiological effect of a A;Reference number: A44921; MUID:92104992; PMID:1729225 A;Contents: AM1 A;Accession: A44921 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-20 <chi>A;Note: sequence extracted from NCBI backbone (NCBIN:75202, 1) C;Keywords: oxidoreductase</chi>		30 18 100.0 96 2 31 18 100.0 96 2 32 18 100.0 98 2 33 18 100.0 99 2 34 18 100.0 99 2 35 18 100.0 101 2 36 18 100.0 102 2 37 18 100.0 104 2 38 18 100.0 107 2 40 18 100.0 107 2 41 18 100.0 108 2 42 18 100.0 108 2 43 18 100.0 109 2 44 18 100.0 109 2 44 18 100.0 109 2 45 18 100.0 109 2
Score 18; DB 2; Length 33; Pred. No. 1.1e+02; 0: Mismatches 0: Indels	scherichia coli -Feb-2001 #text_ V.; Mau, B.; Gl im, A.; Dimalant aggic Escherichia ; PMID:11206551 ; PMID:11206553 bstrain EDL933	Score 18; DB 2; Length 2 Pred. No. 63; 0; Indels	.1.81) - Methylobacterium extor quens ision 18-Nov-1994 #text_change M.E. d physiological effect of a hyo 92104992; PMID:1729225 D:g150010; PIDN:AAA25378.1; PII CBI backbone (NCBIN:75202, NCB	ALIGNMENTS	E81786 T12686 JC2403 S70645 AC1127 AC1127 T35232 S13225 S13225 T17137 T17137 T17856 T16898 T16898 T1786677 T1786677 T1786611
h 33; h 33;	(strain O157:H7, substrain Echange 14-Sep-2001 asner, J.D.; Rose, D.J.; Maja, E.; Potamousis, K.; Apodalcoli O157:H7.	n 20; els 0; Gaps 0;	extorquens (fragment) nange 08-Oct-1999 a hydroxypyruvate reductas		conserved hypothet hypothetical prote PMS8 homolog misma cell division cont hypothetical prote hypothetical prote embryonic abundant hypothetical prote embryonic abundant hypothetical prote phosphoribosyl-ATP hypothetical prote sigma regulatory f sigma regulatory f

Matches

4;

Conservative

0;

Mismatches

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Indels

0;

Gaps

0;

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haptoglobin precursor - bovine (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1992 #sequence_revision 31-
                                                           HPBO
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                                                                                                                                                                                                                                                                                                   A; Experimental
                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-44 <ST2>
                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE005174; NID:g12513992; PIDN:AAG55329.1; A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Z1184 [imported] -
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 1
C;Accession: E85608; F85659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and seven rel A; Reference number: A49410; MUID:94089752; PMID:7903455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
D49410
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A; Residues: 1-44 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Perna, N.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Oryctolagus cuniculus (domestic rabbit) C; Date: 21-Sep-1994 #sequence_revision 18-Nov-1994 C; Accession: D49410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: E85608
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                                                                                                                                                                                                                                                                                              Cross-references: GB:AE005174; NID:912514512; PIDN:AAG55738.1; Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                        Accession: F85659
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#sequence_revision 31-May-1996 #text_change
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Pred. No. 1.5
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli (strain 0157:H7, substrain
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                                                                                                                                                                                                                           Length 44;
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31-Oct-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-Sep-2001
                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                              GSPDB:GN00145;
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K.; Apodaca
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A; Molecule type:
                                                                                                                         R; Lewis, T.L.; Greenberg, H.B.;
J. Virol. 68, 77-83, 1994
A; Title: Analysis of astrovirus
                                                                                                                                                                                       RNA-directed RNA polymerase (EC 2.7.7.48) - human astrovirus type 1 (fragme C;Species: human astrovirus type 1 C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Dec-1994 C;Accession: B49529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Rosidues: 26.45 <MO2>
C;Comment: The matture haptoglobin molecule is a dimer of heterodimers, the two cha C;Comment: Haptoglobin is a plasma glycoprotein; haptoglobin forms a complex with C;Superfamily: haptoglobin; complement factor H repeat homology; trypsin homology C;Keywords: acute phase; glycoprotein, hemoglobin binding; heterotetramer; iron tr F;1-25/product: haptoglobin alpha chain (fragment) #status experimental <ALP>
F;26-45/product: haptoglobin beta chain (fragment) #status experimental <BET>
                          A; Residues: 1-52
                                                                                      A; Accession: B49529
                                                                                                        A; Reference number: A49529;
                                                                                                                                                                                                                                                                                    B49529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squar Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell A;Title: Deciphering the biology of Mycobacterium tuberculosis from the A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Rv1119c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis | C;Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-49 < COL>
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A;Title: Isolation and Characterization of bovine haptoglobin fro A;Reference number: A40430; MUID:91268055; PMID:1904872
A;Accession: A40430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: strain
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R; Morimatsu, M.; Syuto, B.;
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Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin,
J.; Rutter, S.; Seeger, K.; Skelton, S.; Square
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No. 1.6e+02;
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Nakazaki, N.; Shimpo, S.; Sugimoro, m., zuneren.
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DNA Res. 8, 205-213, 2001
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana.
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana.
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana.
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C;Accession: AC2486
C;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S. R;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S. S;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S. S;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S. S;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S. S;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S. S;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S. S;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S. S;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S. S;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S. S;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S. S;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S. S;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S; Namada, M; 
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Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001;
Accession: AB0174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN:CAC90253.1; PID:g15979473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 2;
Pred. No. 1.8e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 2;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 2;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s, the causative agent of plague PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strain PCC 7120
30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                           0;
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Nucleic Acids Res. 28, 2311-2314, 2000

Nucleic Acids Res. 28, 2311-2314, 2000

A; Title: Comparison of whole genome sequences of chlamydia A; Reference number: A86491; MUID:20330349; PMID:10871362
                                                                                                                                                                                                                                                                                                                                                            hypothetical protein CPj0831 [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
밁
                            Qy
                                                                                                                                                                                                                                                           A; Reference number: A; Accession: E86594
                                                                                                                                                                                                                                                                                                                               C;Accession: E86594
R;Shirai, M.; Hiraka
                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-56 <STO>
                                                                                                                                                                         A; Experimental source:
                                                                                                                                                                                           A; Cross references:
                                                                                                                                                                                                                                          A; Status: preliminary
                                                                 Query Match
Best Local S
Matches 4
                                                                                                                                                         Genetics:
 47
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                                                                                                                                       CPj0831
SLDA
                                SLDA 4
                                                               h 100.0%;
Similarity 100.0%;
4; Conservative 0
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                                                                                                                                                                         GB:BA000008; NID:g8979205; ce: strain J138
                                                                                                                                                                                                                                                                                                                                 H.; Kimoto,
                                                                  0;
                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                               M.; Tabuchi,
                                                                  Mismatches
                                                                                    18;
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2e+02;
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                                                                    0
                                                                                                 Length
                                                                                                                                                                                                                                                                                           pneumoniae J138.
                                                                                                                                                                                          GSPDB:GN00142
                                                                 0;
                                                                 Gaps
                                                                  0;
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A;Title: Comparative genomes of Clamydia pneumoniae and C. A;Reference number: A72000; MUID:99206606; PMID:10192388 A;Accession: A72031 C;Species: Chlamydophila pneumoniae, Cl C;Date: 23-Apr-1999 #sequence_revision C;Accession: A72031; D81509 R; Kalman, S.; Mitchell, W.; Marathe, R.; Nature Genet. 21, 385-389, 1999 A; Molecule type: DNA A; Residues: 1-56 < ARN> A;Cross-references: GB:AE001663; GB:AE001363; NID:g4377134; PIDN:AAD18968.1; PID:g437 A; Status: preliminary hypothetical protein CP1039 [imported] - Chlamydophila pneumoniae (strains CWL029 and Chlamydia pneumoniae on 23-Apr-1999 #text_r Lammel, C.; Fan, J.; #text_change 11-May-2000 Olinger, Grimwood, O.; Hicke

A;Experimental source: strain CWL029

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; H.C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Sa Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: D81509

A;Status: preliminary

A; Molecule type: DNA A; Residues: 1-56 < REA> A; Cross-references: GB: AEO02261; GB: AEO02161; A; Experimental source: strain AR39, HL cells Genetics: NID:g7189950; PIDN:AAF38814.1; PID:g718

1 SLDA 4

Local Similarity

100.0%;

Score 18; Pred. No.

DB 2; 2e+02;

Length

56

0

0

Gaps

0;

47 SLDA

50

hypothetical protein CP0758 [imported] - Chlamydophila pneumoniae (strain AR39) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 C;Accession: F81541 RESULT 12

Brunham, R.C.; R.; Gwinn, M.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O. Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; ; Hicke Salzbe

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R;Chen, L.H.; Kenyon, G.L.; Curtin, F.; Harayama, S.; Bembenek, J. Biol. Chem. 267, 17716-17721, 1992

A;Title: 4-Oxalocrotonate tautomerase, an enzyme composed of 62
A;Reference number: A43397; MUID:92388122; PMID:1339435
A;Accession: A43397
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-63 <CHED
A;Residues: 1-63 <CHED
A;Harayama, S.; Rekik, M.
Mol. Gen. Genet. 239, 81-89, 1993
Mol. Gen. Genet. 239, 81-89, 1993
              A;Title: Nucleotide sequence
A;Reference number: S24417; M
                                                                      C; Accession: S24422
R; Shingler, V.; Powlowski, J.;
                                                                                                      C;Species: Pseudomonas putida
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: 4-oxalocrotonate tautomerase C;Keywords: aromatic hydrocarbon catabolism; F;2-63/Product: 4-oxalocrotonate tautomerase F;2/Active site: Pro #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Comparison of the nucleotide sequences of the meta-cleavage pathway genes cleotide substitutions contribute to enzyme evolution.
A;Reference number: S35222; MUID:93288011; PMID:8510667
A;Accession: S35225
A;Molecule type: DNA
A;Residues: 1-63 <HAR>
                                                                                                                                                  4-oxalocrotonate tautomerase (EC 5.3.2.-)
                                                                                                                                                                               S24422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: xylH
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:M94186; NID:g150970; PIDN:AAA25694.1; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4-oxalocrotonate tautomerase (EC 5.3.2.-) xylH - Pseudomonas putida plasmid C;Species: Pseudomonas putida C;Species: Pseudomonas putida C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Mar-2000 C;Accession: A43397; S35225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-62 <REA>
A;Cross-references: GB:AE002235; GB:AE002161; NID:g7189672; PIDN:AAF38560.1; PID:g718967
A;Experimental source: strain AR39, HL cells
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A; Title:
A; Accession:
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                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                        Bacteriol.
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                                                    174, 711-724, 1992
                                                                                                                                                                                                                                                       34
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                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from NCBI backbone (NCBIN:112741, NCBIP:112742)
              e and functional MUID:92121108; I
                                                                        Marklund,
                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                        Score 18; DB 2; Pred. No. 2.3e+02;
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                                                                                                                                                  dmpI [similarity]
                analysis of the complete phenol/3,4-dimethy.
                                                                                                                                                                                                                                                                                                                                                                                                                      intramolecular oxidoreductase;
#status predicted <MAT>
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                                                                                                                                                  Pseudomonas
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                                                                                                              17-Mar-2000
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haptoglobin precursor - rabbit (fragments)
N;Contains: haptoglobin alpha chain; haptoglobin beta
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1988 #seguence_revision 31-May-1996 #te
C;Accession: A19376; A26503
R;Chow, V.; Murray, R.K.; Dixon, J.D.; Kurosky, A.
FEBS Lett. 153, 275-279, 1983
A;Title: Biosynthesis of rabbit haptoglobin: chemical
A;Reference number: A19376; MUID:84005090; PMID:641320
A;Accession: A19376
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 34-73 < KUR>
C; Comment: The mature haptoglobin molecule is a dimer of heterodimers, the two cha C; Comment: Haptoglobin is a plasma glycoprotein; haptoglobin forms a complex with C; Superfamily: haptoglobin; complement factor H repeat homology; trypsin homology C; Keywords: acute phase; glycoprotein; hemoglobin binding; heterotetramer; iron tr
                                                                                                                                 R:Kurosky, A.; Kim, H.H.; Touchstone, B. Comp. Biochem. Physiol. B 55, 453-459, 1976 A;Title: Comparative sequence analysis of the A;Reference number: A90931; MUID:77025019; PMI A;Accession: A26503
                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 1-33 <CH2>
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A;Accession: F84858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
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A; Residues: 1-64 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-63 <SHI>
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Pred. | No. 2.3e+02;
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No.
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70523
A;Accession: E70523
                                                                                                                                                                                                                           R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heide, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolon Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn; A;Reference number: A81500; MUID:20150255; PMID:10684935 A;Accession: A81539
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                                                                                                                                    A;Residues: 1-75 < REA>
A;Cross-references: GB:AE002238; GB:AE002161;
A;Experimental source: strain AR39, HL cells C;Genetics:
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   밁
                                                                                                                                                                                                                                                                                                                           exodeoxyribonuclease, small chain CP078 (Species: Chlamydophila pneumoniae, ChC;Bpecies: Amar-2000 #sequence_revision C;Accession: A81539
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C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998
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A; Residues: 1-73 <COL>
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4; Conservative
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4; Conser
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ce: strain |
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H37Rv
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31-Mar-2000 #text_change 11-May-2000
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A; Molecule type: A; Residues: 1-87
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R;Tomaschewski, J.; Rueger, W. Nucleic Acids Res. 15, 3632-3633, 1987 Nucleic Nucleotide sequence and primary structures of A;Title: Nucleotide sequence and primary structures of A;Reference number: A30291; MUID:87203398; PMID:3575111 A;Accession: F30292
                                                                                     A; Note: host Escherichia coli
C; Date: 31-Dec-1989 #sequence_revision
C; Accession: F30292
                                                                                                                                        gene 55.1 protein
C; Species: phage 5
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A; Residues: 1-85 <KLE>
A; Cross-references: GB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, Smith, H.O.; Woese, C.R.; Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision
C;Accession: A69435
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A; Title: Complete genome sequence of the alkaliphilic bacterium A; Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision
C;Accession: G8935
C;Accession: G8935
R;Takami, H; Nakasone, K; Takaki, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: The complete genome sequence of the hyperthermophilic, A; Reference number: A69250; MUID:98049343; PMID:9389475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06006.1; A;Experimental source: strain C-125
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A; Residues: 1-76 <STO>
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llarity 100.0%;
Conservative
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Pred. No. 2.8
0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                               Pred. No. 3.1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
                                                                                                       31-Dec-1989 #text_change
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hes 0;
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G.; Gill, S.; Kirkness,
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                                                                                                         23-Jul-1999
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                                      for
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DNA <TOM>

GB:Y00122;

NID: g15346; PIDN: CAA68320.1;

PID:g15362

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: E84162
R:N9, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, J. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jab Jung, K.H.; Alam, M.; Freitas, T. 12176-12181, 2000
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: E84162
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A;Gene: 55.
C;Superfami
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                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-88 < KUR>
                                                                                                                                                                                                                                                                                                                      R;Goodner, B.; Hinkle, G.; Gattung, S.;
A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                      R; Goodner, B.;
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C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-87 <STO>
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Best Local
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24
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tes 4; Conserv
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Pred. No.
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. 3.2e+02;
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                                                                                                                                                                                                           PID:g15154992;
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Markelz, B.
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   A; Reference number: A; Accession: T09285
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embryonic abundant protein EMB44 - white spruce (; Species: Picea glauca (white spruce) | C;Date: 11-Jun-199 #sequence_revision 11-Jun-19 (; Accession: T09285 | R;Dong, J.Z.; Dunstan, D.I. submitted to the EMBL Data Library, June 1996 A;Description: Gene expression during somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of the EMBL Data Library (somatic en A;Reference number: Z16588 | Proceedings of th
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A; Residues: 1-88 < KUR>
A; Cross-references: GB: AE008688; PIDN: AAL41144.1; PID: g17738440; GSPDB: GN00186
A; Experimental source: strain C58 (Dupont)
C; Genetics:
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C; Superfamily:
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C; Accession: An2591
C; Accession: An2591
C; Accession: An2591
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wooderage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClerage, F.; Romero, P.; Zhang, S.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-90 < PRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain
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C;Date: 21-Jan-2000 #sequence_revision
C;Accession: T44780
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A; Map position: circular
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Pred. No.
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3.3e+02;
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                                       embryogenesis
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conserved hypothetical protein NMB0343 [imported] - Neisseria meningitidis (strain MC C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: B81209 R;Tettelin: H; Saunders, N.J.; Heldelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, H;Ckey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. K.; Oli, H; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein - white spruce C; Species: Picea glauca (white spruc C; Date: 11-Jun-1999 #sequence_revisi C; Date: 11-Jun-1999 #sequence_revisi C; Accession: T09293 R; Dong, J.Z.; Dunstan, D.I. Planta 199, 459-466, 1996
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A; Residues: 1-91 <DON>
A; Cross-references: EMBL:L47750; NID:g1350537;
C; Genetics:
A; Gene: EMB44
C; Superfamily: embryonic abundant protein Em
                                                                                                                                                                                                                                                             A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; MA;Title: Complete genome sequence of Neisseria meningitidis A;Reference number: A81000; MUID:20175755; PMID:10710307 A;Accession: E81209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-reference: ____C;Superfamily: embryonic
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                                                                                                                                                           A; Experimental source: C; Genetics:
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A:Experimental source: serogroup
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A; Residues: 1-91 <DON>
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A; Residues: 1-92 <TET>
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                                                                                                                                                                                                                                              A;Status: preliminary
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                                                                                                     Query Match
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29 SLDA 32
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SLDA 63
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B, strain MC58
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Pred. No.
                                                                  Score 18; DB 2;
Pred. No. 3.4e+02;
; Mismatches 0;
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Pred. No.
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MC58.
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hypothetical protein 63B12.12 - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-C;Accession: T12686 R;Ferraz; C; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G. submitted to the EMBL Data Library, January 1998 A;Description: Sequencing the distal X chromosome of Drosophila mel. A;Reference number: Z17572
                                                                                                                                                                                                                           RESULT
T12686
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A; Residues: 1-96 < PAR>
A; Cross-references: GB
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T10931
A; Molecule type: DNA
A; Residues: 1-96 <FER>
                                                     A; Reference number: A; Accession: T12686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000
C;Accession: E81786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribosomal protein S15 - Streptomyces coelicolor C; Species: Streptomyces coelicolor
                                 A; Status: preliminary; translated
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A; Residues: 1-95 < PA
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A; Accession: T10931
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                                                                                                                                                                                                                                                                                                        64 SLDA
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                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli ribosomal protein S15; eubacterial ribosomal protein eubacterial ribosomal protein S15 homology <S15>
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source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                              100.0%;
ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB85356.1; PID:g738
                                                                                                                                                                  #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
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                                     from
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Pred. No. 3.6e+02;
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                                   GB/EMBL/DDBJ
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Moule, S.;
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1998
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Mungall, K.; Quail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 95;
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                                                                                            melanogaster
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M.A.;
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Rajandre
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22

EMBL:AL021106; NID:e1371406; PID:e1226203; PIDN:CAA15943.1

clone

cosmid 63B12

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cell division control protein CKS1 - Leishmania mexicana N;Alternate names: protein pl2LmmCKS1; protein pl3sucl homolog C;Species: Leishmania mexicana C;Cate: L4-Feb-197 #sequence_revision 13-Mar-1997 #text_change C;Accession: S70645; S57414 R;Mottram, J.C.; Grant, K.M. Biochem. J. 316, B33-839, 1996 A;Title: Leishmania mexicana pl2cks1, a homologue of fission yea: A;Reference number: S70645; MUID:96265049; PMID:8670159 A;Molecule type: DNA A;Residues: 1-99 <MOT>
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                                                                                                                                                                       A;Cross-references: EMBL:Z49881; C;Genetics:
                                                                                                                                                          A; Gene: cks1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Gene: GDB:PMS2L6; PMS8
A;Cross:references: GDB:437147
A;Map position: 7q11.23-7q22
C;Keywords: DNA repair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-98 <HOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: JC2403
R;Horil, A.; Han, H.J.; Sasaki, S.; Shimada, M.; Nakamura, Y.
Biochem. Biophys. Res. Commun. 204, 1257-1264, 1994
A;Title: Cloning, characterization and chromosomal assignment of A;Reference number: JC2398; MUID:95071462; PMID:7980603
A;Accession: JC2403
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A; Introns: 27/1
A; Note: 63B12.12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date:
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                                                          Matches
                                                                                                                     ;Superfamily: cell division control protein ;Keywords: cell cycle control
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Matches
                                                                            Query Match
Best Local
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;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 05-Nov-1999
;Accession: JC2403
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11
                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 SLDA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 SLDA
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                            SLDA 4
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Similarity 100.0%;
4; Conservative 0
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                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase:FBgn0000117
                                                                       100.0%;
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                                                                                                                                                                               NID: g871408; PIDN: CAA90037.1;
                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                       Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 2;
Pred. No. 3.7e+02;
""smatches 0;
                                                                        Pred.
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Pred. No.
                                                     Mismatches
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                                                     . 3.7e+02;
thes 0;
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ches 0;
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                                                     Indels
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                                                                                                                                                                                                                                                          associates
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hypothetical protein SC5C7.25 SC5C7.25 - Streptomyc C; Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 C;Accession: T35232
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T35232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein lin0439 [imported] Listeria innocua (strain Clip11262) (;Species: Listeria innocua C;Species: Listeria innocua C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AH1487 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Jones, L.M.; Karst, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669. A;Accession: AH1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-99 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AL592022; PIDN:CAC95672.1; PID:g16412868; GSPDB:GN00178
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 294, 849-852,
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 35
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A;Experimental source: strain EGD-e
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A; Residues: 1-99 <GLA>
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Best Local
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                                                    D.,
                                                                                                                                                                                                                                                                                                                                     100.0%; Score 18; DB 2; L
100.0%; Pred. No. 3.7e+02;
^. Mismatches 0;
                          Parkhill, J.; Barrell,
Library, September 1998
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                                                                                                                                     Streptomyces
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3.7e+02;
1es 0;
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Vazquez-Boland, J.A.;
                                          B.G.; Rajandream, M.A.
                                                                                        #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                     Length 99;
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Voss, H.; Wehla
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Fsihi,
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submitted to the EMBL Data Library, December 1995
A;Description: Determination and analysis of the col
A;Reference number: 222022
A;Accession: T41937
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-104 <NIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              embryonic abundant protein D-19 - upland cotton W;Alternate names: lea protein D-19 C;Species: Gossypium hirsutum (upland cotton) C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1 C;Accession: S19225; S04041 R;Dure III, L.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
S19225
A; Experimental source: strain JI C; Genetics: A; Note: U35
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A;Residues: 1-101, 'KLNIISHDRTLATPFIYKP'
A;Cross references: EMBL:X13205
A;Note: this sequence has been revised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:x13205; NID:g18493; PIDN:CAA31593.1; PID:g18494 R;Baker, J.; Steele, C.; Dure III, L. Plant Mol. Biol. 11, 277-291, 1988 A;Title: Sequence and characterization of 6 Lea proteins and their genes
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A;Molecule type: DNA
A;Residues: 1-101 <SEE>
A;Cross:references: EMBL:ALO31515; PIDN:CAA20637.1;
                                                                                                                                                                                                               R; Nicholas, J.
                                                                                                                                                                                                                               C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T41937
                                                                                                                                                                                                                                                                     C; Species: human herpesvirus A; Variety: strain JI
                                                                                                                                                                                                                                                                                               hypothetical protein U35 - human herpesvirus C:Species: human herpesvirus 7
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T41937
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A; Accession: S04041
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A; Residues: 1-102 <BAK1>
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                                                       A; Cross-references: EMBL: U43400; PIDN: AAC54697.1
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Gene: SCOEDB:SC5C7.25
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Pred. No. 3.9e+02;
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3.8e+02;
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Apporthetical protein 108 - Cyanophora paradoxa cyanelle CySpecies: cyanelle Cyanophora paradoxa C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #texic:Accession: T06898
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T17856
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H87712
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R;Graves, M.V.; Van
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C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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C; Superfamily:
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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A;Experimental source: specific host Chlorella strain NC64A
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A; Accession: T17856
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A;Molecule type: DNA
A;Residues: 1-107 <STO>
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C;Accession: H87712
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                                                                                      RESULT 41
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Pred. No.
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Pred. No.
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Pred. No. 3.9e+02;
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Bohnert,

H.J.; Bryant, D.A.

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awa, H.; Takamıya, M.; Masumu, J., John Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72641
A;Status: preliminary
                                                                                    A; Status: FLOWER DNA
A; Molecule type: DNA
A; Residues: 1-109 < KAW>
A; Cross-references: DDBJ: AP000060;
A; Cross-references: Strain K1
                                                                                                                                                                                                                                                                  R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.;
awa, H.; Takamiya, M.; Masuda, S.; Funahash
                                                                                                                                                                                                                                                                                                         hypothetical protein APE0568 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: H72641
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submitted to the EMBL Data Library, July 1995
A;Description: Nucleotide sequence of the cyanelle genome
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 43
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A;Experimental source: strain A3(2)
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A; Residues: 1-108 <SAU>
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A; Residues: 1-108 <STI>
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Gene: SCOEDB:SC1A9.28c
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i, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
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R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, Nuccleic Acids Res. 28, 2311-2314, 2090 Res. 28, 7311-2314, 2090 Res. 28, 7311-2314, 2090 Research A;Reference number: A86491; MUID:20330349; PMID:10871362
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C;Superfamily:
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A;Residues: 1-110 <ARN>
A;Cross-references: GB:AE001671; GB:AE001363;
A;Experimental source: strain CWL029
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RESULT 2
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DMPI_PSESP STANDARD; PRT; 62 AA. P49172; 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)

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Best Local
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01-JUL-1993
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                                                                                                                                                                      XYLH
SEQUENCE FROM N.A.,
STRAIN=mt-2;
                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
SEQUENCE
                                                                                    Pseudomonas
                                                                                                                                Plasmid
                                                                                                                                                Pseudomonas
                                                                                                                                                                                       4-oxalocrotonate tautomerase
                                                                                                                                                                                                                                                                              Q01468;
                                                                                                                                                                                                                                                                                                XYLH_PSEPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Bacteria; Protect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson K.S., Wigley D.B.;
"Enzymatic ketonization of 2-hydroxymuconate: specificity and mechanism investigated by the crystal structures of two isomer Biochemistry 35:792-802(1996).

-I- FUNCTION: CATALYZES THE KETONIZATION OF 2-HYDROXYMUCONATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD019232; Tautomerase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X60835; CAA43229.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Subramanya H.S., Roper D. Wilson K.S., Wigley D.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=96146412; PubMed=8547259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequence and functional phenol/3,4-dimethylphenol catabolic strain CF600.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       somerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=92121108; PubMed=1732207;
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(Rel.)
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                                                                                                                                                                                                                                                                                                STANDARD;
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38,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6974 MW;
             AND SEQUENCE OF 1-33.
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0 BY SIMILARITY.
1 CATALYTIC BASE (BY SIMILARITY).
6974 MW; CEDABOF92DIEIEOF CRC64;
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functional analysis of the complete
catabolic pathway of Pseudomonas sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18; DE Pred. No. 1.2); Mismatches
                                                                                                                                                                                                                                                                                           PRT;
                                                                                               subdivision;
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                                                                                          Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage
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                                                                                                                                                                              INIT_MET ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR, AND ACTIVE SITE. MEDILINE-9616413; PubMed-8547260; Stivers J.T., Abeygunawardan C., Mildvan A.S. Whitman C.P., Chen L.H.; Catalytic role of the amino-terminal proline Catalytic role of the amino-terminal proline.
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                                                                                                                                                                                                                                                                                      'IGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hackert M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taylor A.B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Crystal structure of 4-oxalocrotonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98453316; PubMed=9778344;
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Wilson K.S., Wig
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Chen L.H., Kenyon G.L., Curtin F.,
Hajipour G., Whitman C.P.;
"4-oxalocrotonate tautomerase, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93288011;
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                                                                                                                                                                                                                                                                       TIGR00013; taut;
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100.0%;
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                                                                                                                                                                                                                                                                                                        Tautomerase; 1.
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                                                                                                                                           M.
                                                                                                                            CATALYTIC BASE.
23E6DC494A12254F CRC64;
                                                                                                                                                                                                                                       hydrocarbons
                            Score 18;
Pred. No.
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                                                                                                                                                                                                                                    catabolism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jr.,
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Similarity 4; Conserv

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No. 1.2e+02;

DB 1;

Length 62;

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SLDA |||| SLDA

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RESULT 4
EX7S_CHLPN
                                  EMBL; AE001686; EMBL; AE002238; AE002548; EMBL; AP002548; TIGR; CP0788; -
                                                                                                                                                                                                                                 Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. tra Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable exodeoxyribonuclease VII small subunit
(Exonuclease VII small subunit),
XSEB OR CPNI061.1 OR CP0788.
                                                                                             use by non-profit institutions as long modified and this statement is not removed: entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gwinn M., Nelson W., DeBoy R., Kolonay J.,
Elsen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis
pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White O., Hickey E.K., Peterson J., Utterback T., Berry Linher K., Weldman J., Khouri H., Craven B., Bowman C., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EX7S_CHLPN
Q9K1Y4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                SUBCELLULAR SIMILARITY:
                                                                                                                                                                                                                           SIMILARITY).
         IPR003761; Exonuc_VII_S.
2609; Exonuc_VII_S; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                          -; NOT_ANNOTATED_CDS.
AAF38587.1; -.
                                                                                                                                                                                               LOCATION: Cytoplasmic (By similarity).
BELONGS TO THE XSEB FAMILY.
                                              -; NOT_ANNOTATED_CDS
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y K., Bass S.,
, Dodson R.,
, Salzberg S.L.,
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RESULT 5
GP56_BPSP1
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Matches 4
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O48410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-98327781; PubMed-9657951;

Stewart C.R., Gas11qhtwala I., Hinata K., Krolikowski K.A.,

Stewart C.R., Gas11qhtwala I., Hinata K., Krolikowski K.A.,

Needleman D.S., Peng A.S.-Y., Peterman M.A., Tobias A., Wei P.;

"Genes and regulatory sites of the 'host-takeover module' in the

terminal redundancy of Bacillus subtills bacteriophage SPOl.";

Virology 246:329-340(1998).
                         SEQUENCE FROM N.A. STRAIN-VC-16 / DSN
                                                          Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeog
Archaeoglobaceae; Archaeoglobus
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                             EMBL; AF031901; AAC29025.1; Hypothetical protein. SEQUENCE 79 AA; 9305 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses.
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Viruses; dsDNA viruses,
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            STRAIN=VC-16 / DSM 4304 / ATCC 49
MEDLINE=98049343; PubMed=9389475;
                                                                                                                            Hypothetical
                                                                                                                                        16-0CT-2001
16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10685;
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15-DEC-1998
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(Rel. 37, Last sequence up)
(Rel. 37, Last annotation)
ne protein 56.
                                                                                                                           (Rel. 40, Created)
(Rel. 40, Last sequence update)
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protein AF1482.
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                                                                                     Archaeoglobi; Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              no
                         ATCC 49558;
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 Tomb J.-F.,
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Pred.
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Pred. No.
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White O.,
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1.5e+02;
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 Nelson K.E.,
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RESULT 7
YOUA_BPT4
ID YOUA_BPT4
AC P07083;
DT 01-APR-1988 (
DT 01-APR-1988 (
DT 15-JUN-2002 (
DE HYPOTHETICAL
GN YOUAO OR 55.1.
OS Bacteriophage
OC Viruses; dsDN
OC T4-like virus
OX NCBI_TaxID=10
RN 121
RP SEQUENCE FROM
RN 121
RP SEQUENCE FROM
RN 101
RP SEQUENCE FROM
RN 101
RP SEQUENCE FROM
RN 101
RP TOMBASCHEWSL
RT NUCLECT ACIDS
RN 121
RY MEDLINE-67207
RA MUTTER P. ALI
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                              Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                           Kutter E., Arisaka F., Kunisawa T., Tsugita A
Mesyanzhinov V., Ruger W., Stidham T., Thomas
"Bacteriophage T4 genome analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence and primary structures of gene products confor by the T4 genome between map positions 48.266 kb and 39.166 Nucleic Acids Res. 15:3632-3633(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage T4.
Viruses; dsDNA viruses,
T4-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Iomaschewski J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-87203398; PubMed=3575111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caudovirales; Myoviridae;
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Best Local S
Matches 4
                                                                                                                                RS15_STRCO STANDARD;

08655;

30-MAY-2000 (Rel. 39, C);

30-MAY-2000 (Rel. 41, L);

15-UN-2002 (Rel. 41, L);
                                                                                                                                                                                                                                                  _STRCO
                                                              Streptomyces coelicolor.
Bacteria; Actinobacteria
                                                                                                15-JUN-2002 (Rel. 41, Last annotation 30S ribosomal protein S15. RPSO OR SC05736 OR SC3C3.22.
                     Actinomycetales; Streptomycineae;
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMI_PICGL STANDARD; PRT; 91 AA. Q40864; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000389; Seed_protein.
Pfam; PF00477; seed_protein; 1.
PROSITE; PS00431; SMALL_HYDR_PLANT_SEED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L42464; AAA85366.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dong J.Z., Dunstan D.I., Submitted (JAN-1996) to -1- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Picea glauca (White spruce).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
NCBI_TaxID=3330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Em-like protein
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EMBL; AF158101; AAD42492.1;
PIR; F30292; ZGBPT9.
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29 SLDA 32
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nes 4; Conserv
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                                                       Actinobacteria; Actinobacteria (class);
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91 AA;
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Pred. No. 1.9e+02;
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RESULT 10
ES98_DROME
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ID 9828_B
ID 9828_B
ID 9828_B
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ID 1
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InterPro; IPR005290; RS15_bact.
InterPro; IPR00589; Ribosomal_S15.
InterPro; IPR000589; Ribosomal_S15; 1.
Pfam; pP00312; Ribosomal_S15; 1.
TIGRFAMS; TIGR00952; S15_bact; 1.
PROSITE; PS00362; RIBOSOMAL_S15; 1.
PROSITE; PS00362; RIBOSOMAL_S15; 1.
Ribosomal protein; TRNA-binding; Complete proteome.
Ribosomal protein; TRNA-binding; Complete proteome.
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Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                    STRAIN-Berkeley;
MEDLINE=20196006; PubMed=10731132;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Eukaryota; Metazoa; Arthropoda; Endopterygota; Diptera; Brachycera;
Insecta; Pterygota; Neoptera; Endopterygota; Drosophila.
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Nature 417:141-147(2002)
-i- FUNCTION: THIS PROTEIN IS ONE PROTEINS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ES98_DROME STANDARD; PRT; 96 AA 097420; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat EST00098 protein homolog EG:63B12.12 OR CG14818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extended the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL031231; CAA20271.1; HSSP; P80378; 1AB3.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Similarity 100.0%;
4; Conservative 0;
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                                                                                                                                               RA Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liu X., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McRulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McHalov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Muzny D.R., Pacleb J.M.,
RA Mount S.M., Melson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pithman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.M., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Schence 287:2185-2195(2000).
                                               Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-Oregon-R;

MEDLINE-20196011; PubMed-10731137;

MEDLINE-20196011; PubMed-10731137;

Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,

Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu I

Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova

Minana B., Kafatos F.C., Louis C., Siden-Klamos I., Bolshakov S.,

Papagiannakis G., Spanos L., Cox S.; Madueno E., de Pablos B.,

Modolell J., Peter A., Schoettler P., Werner M., Mourkloti F.,

Beinert N., Dowe G., Schaefer U., Jacekle H., Bucheton A.,

Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,

McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,

Glover D.M.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "From sequence to chromosome: the tip of the a chilomosome melanogaster."; Science 287:2220-2222(2000).
-!- SIMILARITY: BELONGS TO THE UPF0184 (EST00098) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandr Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davries P., de Pablos B., Delcher A., Deng Z., Ways A.D., Dew I., Dietz S.M. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Du Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischma Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                   Hypothetical protein;
DOMAIN 21 7
                                                                                                                                                                                                                                                                                     EMBL; AE003422; AAF45682.1; -. EMBL; AL021106; CAA15943.1; -.
                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                  Pfam; PF03670; UPF0184;
                                                                                                                                                                                                                                      FlyBase; FBgn0026088; EG:63B12.12.
InterPro; IPR005374; UPF0184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
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Butler H.,
                                                 0
                                                                                                                                          coil.
COILED COIL (POTENTIAL).
98452A2233F231BF CRC64;
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                                                 Mismatches
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                                                                       2e+02;
                                                                                           1; Length 96;
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RESULT 11
CKS1_LEMME
ID CKS1_
AC Q253;
DT 01-N(

        PHS_STAC

ID _PHS_S

AC 08672

DT 16-0C

DT 16-0C

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Best Local
                                                                                                            Streptomyces coelicolor.
Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae;
Pacteria; Actinobacteria; Streptomycese; Streptomycese; Streptomyces.
                                                                                                                                                                                                                                                                PHS_STRCO STANDARD; PRT; 101 AA.
086772;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative pterin-4-alpha-carbinolamine dehydratase (EC 4.2.1.96) (PHS)
(4-alpha-hydroxy-tetrahydropterin dehydratase) (Pterin carbinolamine
SEQUENCE FROM N.A.
STRAIN-A3(2) / M145;
MEDLINE-21996410; PubMed-12000953;
                                                                                                                                                                                                                                  SC06540 OR SC5C7.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Q25330;
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00296; CYCLINKINASE.
ProDom; PD005152; Cyc_dep_kin_rsub;
PROSITE; PS00944; CKS_1; 1.
PROSITE; PS00945; CKS_2; 1.
Cell division.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000789; Cyc_dep_kin_rsub.
Pfam; PF01111; CKS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z49881; CAA90037.1; -. HSSP; P33551; 1BUH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           associates with a stage-regulated histone Biochem. J. 316:833-839(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Cyclin-dependent kinases regulatory subunit (P12LMMCKS1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leishmania mexicana.
Eukaryota; Euglenozoa; Kinetoplastida;
NCBI_TaxID=5665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: BINDS TO THE CATALYTIC SUBUNIT OF THE CYCLIN DEPENDENT KINASES (CDC2) AND IS ESSENTIAL FOR THEIR BIOLOGICAL FUNCTION. SUBUNIT: FORMS AN HOMOHEXAMER THAT CAN PROBABLY BIND SIX KINASE SUBUNITS (BY SIMILARITY).

SUBUNITS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLDA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
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100.0%; F
itive 0;
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Pred. No. 2e+02;
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kinase.";
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RESULT 13
LE19_GOSHI
ID LE19_GOSHI
          В
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Best Local
SEQUENCE FROM N.A.
Galau G.A., Wang H.Y., Hughes D.W.;
Galau G.A., Wang H.Y., Hughes D.W.;
Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: LEA PROTEINS ARE LATE EMBRYONIC PROTEINS ABUNDANT
HIGHER PLANT SEED EMBRYOS. THERE ARE TWO SUBSETS OF LEA PROT
                                                                                                    Dure L. II Submitted
                                                                                                                                                                                                                                                                                                                                               p09443;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Late embryogenesis abundant protein D-19 (LEA
                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                            Gossypium hirsutum (Upland cotton) Eukaryota; Viridiplantae; Streptop
                                                                                                                                                                   Plant
                                                                                                                                                                                     cotton.
                                                                                                                                                                                                              STRAIN=cv. Coker 201;
Baker J., Steele C., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).

'I CATALYTIC ACTIVITY: (6R)-6-(L-erythro-1,2-dihydroxypropyl)-5,6,7,8-tetrahydro-4a-hydroxypterin = (6R)-6-(L-erythro-1,2-dihydroxypropyl)-7,8-dihydro-6H-pterin + H(2)O.

-i- SIMILARITY: BELONGS TO THE PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                   REVISIONS
                                                                                                                                                                                                 "Sequence
                                                                                                                                                                                                                                                                              NCBI_TaxID=3635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M. Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S. Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J., Hopwood D.A.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001533; Trans_pterinDh.
Pfam; PF01329; Pterin_4a; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL031515; CAA20637.1; HSSP; P80095; 1DCO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 SLDA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the ENEuropean Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content
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PD007262; Trans_pterinDh; 1
tical_protein; Lyase; Comple
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                                                                                                    (JAN-1992)
                                                                                                                                                                                              Steele C., Dure L. II and characterization
                                                                                                                                                                   Biol.
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'; DB175F371A11C159 CRC64;
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Pred. No. 2.1e+02;
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                                                                                                                                                                                               of 6 Lea
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OF LEA PROTEINS

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                                                                                                                                                                                                          REDUENCE FROM N.A.

8 SEQUENCE FROM N.A.

8 CSTRAIN-ATCC 19089 / CB15;

8 MEDLINE-21173698; PubMed-11259647;

8 Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.

8 A Lisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

8 A Lisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Haft D.H.,

9 A Notocka I., Nelson W.C., Newton A.S., Gwinn M.L., Haft D.H.,

8 A Notocka I., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

8 A Notocka I., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

8 A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.

8 A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.

8 A Kolonay J.F., Smit J., Craven M.B., Khouri H., Ermolaeva M., White

8 A Liberg S.L., Venter J.C., Shapiro L., Fraser C.M.,

8 A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,

8 Proc. Matl. Acad. Sci. U.S.A. 98:4136-4141(2001).

8 Proc. Matl. Acad. Sci. U.S.A. 98:4136-4141(2001).

9 Phosphoribosyl)-AMP + diphosphate.

1 - PATHWAY: Histidine biosynthesis; second step.
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Best Local
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EMBL; X13205; CAA31593.1; -.

EMBL; M73751; AAA33062.1; -.

EMBL; M73752; AAA33060.1; -.

PIR; S19225; S19225.

InterPro; IPR000389; Seed_protein.

Pfam; PF00477; seed_protein; 1.
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SEQUENCE
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                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat)
Phosphoribosyl-ATP pyrophosphatase (EC 3.6.
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INDUCTION: BY ABSCISTC ACID (ABA),
MISCELLANEOUS: THIS IS A SET 5B PROTEIN.
SIMILARITY: BELONGS TO THE SMALL HYDROPHILIC PLANT S
European Bioinformatics Institute.
by non-profit institutions as laified and this statement is not removed.
                                                                                                                                                                    SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: BELONGS TO THE PRA-PH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR CC3738.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subdivision; Caulobacter group;
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There are no restrictions on it ng as its content is in no ved. Usage has
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s 0;
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M., White O.,
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В Qy

40 SLDA 43

μ. SLDA 4

Query Match Best Local Matches

Similarity

100.0%;

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Score 18; DB 1; Pred. No. 2.2e+02; Mismatches 0;

Length 108; CRC64

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RESULT 15
YC50_CYAPA
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01-FEB-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                      STRAIN=LB555 / Pringsheim;
Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella Loeffelhardt W., Schluchter W.M., Chung S., Newmann-Spallart C., Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
"The complete sequence of the cyanelle genome of Cyanophora the genetic complexity of a primitive plastid.";
the genetic complexity of a primitive plastid.";
(In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E., Schwemmler W. (eds.);
  Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Histidine biosynthesis; Hydrolase; Complete proteome. SEQUENCE 107 AA; 11037 MW; 93280F1FAA8629ED CRC64;
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                                                                                                or send
                                                                                                                         entities requires a
                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                           between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Mol.
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-LB555 / Pringsheim;
Stirewalt V.L., Michalowski C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                             EMBL; U30821; AAA81241.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2762;
                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE YCF50 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leotide sequence of the cyanelle DNA from Cyanophora paradoxa."; t Mol. Biol. Rep. 13:327-332(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYAPA
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                                                                                           s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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                      protein;
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                         Cyanelle.
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Last annotation
protein ycf50 (
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                                                                                                                                             yright. A content is in institute. There are no restrictions of Bioinformatics and the content is in and for content in the content is in the content in the
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Pred. No. 2.2
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RA Spoures J., Peat N., Hayles M., Lyne M., Lyne M., Lyne M., Stewart A., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA James K., Sones M., Leather S., McDonald S., McLean J., RA McOney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., RA Giller K., Ratherford K., Rutter S., Saunders D., Quail M.A., Rabbinowitsch E., RA Woodward J., Volckaert G., Aert R., Squares S., Stevens K., Sharp S., RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Whitehead S., RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Ra Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., RA Gailbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Sharp S., Cruzado L., Jimenez J., Sanchez M., Garzon A., Thode G., RA Gailbert F., McCambie W.F., Paulsen I., Potashkin J., Ra Bonito J., McCambie W.R., Paulsen I., Potashkin J., Thode G., Pive G., Martin B., Potashkin J., Wartren S., Armstrong J., Forsburg S.L., Mature 415:871-880(2002).

C. Synthesis of Very-Long-Chank Fafty Acids (By Similarity).

C. SUBUNIT: Complex I Is Composed of About 30 Different Subunits.

C. Subunits: Complex I Is Composed of About 30 Different Subunits.

C. Subunits: Complex I Is Composed of About 30 Different Subunits.

C. Subunits: Composed of About 30 Different Subunits.
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ACPM_SCHPO
EMBL; Z69380; CAA93348.1; -.

HSSP; P02901; lACP.
InterPro; IPR003231; Acyl_carrier.
InterPro; IPR003880; Ppantine_attach.
Pfam; PF0050; pp-binding; 1.
ProDom; PD000887; Acyl_carrier; 1.
PIGRRAMS; TIGR00517; acyl_carrier; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
Hypothetical protein; Fatty acid biosynthesis; Phosphopantetheine; Mitochondrion; Transit peptide; Oxidoreductase.
TRANSIT 1 28 MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative acyl carrier protein, mitochondrial pubiquinone oxidoreductase 9.6 kba subunit).
SPACH3.09.
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01-0CT-1996
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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S., Basham D., Bowman S.,
Sworth T., Churcher C.M.,
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Matches
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HSSP; P027784; 1PDC.
InterPro; IPR000562; FN_Type_II.
Pfam; PF00040; fn2; 2.
PRINTS; PR00013; FNTYPEII.
PRODom; PD000995; FN_Type_II; 2.
SMART; SM00059; FN2; 2.
PROSITE; PS00023; FIBRONECTIN_2; 2.
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 Y998_RHIME
Q52966;
30-MAY-2000 (
30-MAY-2000 (
15-JUN-2002 (
Hypothetical
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SEQUENCE
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fibronectin.";

fibronectin.";

Biochem. J. 243:195-203(1987).

-i. FUNCTION: THE BSP-A PROTEINS FROM SEMINAL PLASMA EXHIBIT BOTH

SIMULATORY AND INHIBITORY ACTIONS ON THE RELEASE OF PITUITARY

GONADOTROPINS. THE EXACT FUNCTION OF THESE PROTEINS IS NOT KNG

GONADOTROPINS. THE EXACT FUNCTION OF THESE PROTEINS.
                                                                                                                                                                                                                                                      Semen; Plasma;
DOMAIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-87270621; PubMed=3606570; Sairam Seidah N.G., Manjunath P., Rochemont J., Sairam "Complete amino acid sequence of BSP-A3 from bov Homology to PDC-109 and to the collagen-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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13-AUG-1987 (Rel.
01-OCT-1996 (Rel.
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P04557;
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43
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112 AA;
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Conservative 0
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15 AA; 13410 MW;
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Pred. No.
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Pred. No.
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                   update)
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2.3e+02;
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CRC64;
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P44181;
01-NOV-1995
01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Boutry M., Cadleu E., Dreano S., Gloux S Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Penard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the Chromosome sequence of the legume symbiont Sinorhizobium mellloti strain 1021."; Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R00998 OR
Rhizobium
STRAIN-Rd / KW20 / ATCC 51907;
STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O.,
Kerlavage A.R., Bult C.J., Tomb J.-F.,
                                                                                                                                                                                                                                                    HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL591785; CAC45570.1; -.
InterPro; IPR005133; PhaG_mnhG_YufB.
Pfam; PF03334; PhaG_mhhG_YufB; 1.
TIGR01300; CPA3_mnhG_phaG; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 116 AA; 12373 MW; 16F4C117E81C4D10 CRC64;
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Keller M., Roxlau A., Weng W.M., Schmidt M., (
Jording D., Arnold W., Puehler A.;
"Molecular analysis of the Rhizobium meliloti
blosynthesis of the exopolysaccharides succinc
                                                                                                                                                  Hypothetical HI1406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L37353; AAA74238.1; -. EMBL; AL591785; CAC45570.1;
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                     Bacteria;
                                                                                                                                 Haemophilus
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0 SLDA 63
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(Rel.
(Rel.
                                                                                                                                 influenzae.
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(Rel. 41, Last annotation
protein HI1406.
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                                                                                                                    gamma subdivision; Pasteurellaceae;
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Pred. No. 2.4e+02;
; Mismatches 0;
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Dougherty B.A., Merrick
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RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                     "Five crustacean hyperglycemic family hormones of Penaeus monodon: complementary DNA sequence and identification in single sinus glands by electrospray ionization-Fourier transform mass spectrometry."; Mar. Biotechnol. 2:80-91(2000).

-i- FUNCTION: ABUNDANT HORMONE IN THE SINUS GLAND OF ISOPODS AND DECAPODS WHICH CONTROLS THE BLOOD SUGAR LEVEL. HAS A SECRETAGOGUE DECAPODS WHICH CONTROLS THE BLOOD SUGAR LEVEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHH4_PENMO 097386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical SEQUENCE 1:
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Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crustacean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U32820; AAC23056.1; -. TIGR; HI1406; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHH4.
Penaeus monodon (Penoeid shrimp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davey M.L., Hall M.R., Willis R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=10804243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Eyestalk;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6687;
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                                                                                                                                                                                                                                                     WHICH CONTROLS THE BLOOD SUGAR LEVEL. HAS A SECRETAGOGUE ACTION OVER THE ANYLASE RELEASED FROM THE MIDGUT GLAND. MAY ACT AS A STRESS HORMONE AND MAY BE INVOLVED IN THE CONTROL OF MOLTING AND REPRODUCTION (BY SIMILARITY).

SIMILARITY: BELONGS TO THE ARTHBOOD.
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1 (Rel. 40, Last annotation update)
hyperglycemic hormone 4 precursor
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118 AA; 1:
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13325 MW; C1CAF33E6CBB3452 CRC64;
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Pred. No. 2.4e+02,
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Best Local s
Matches 4
InterPro; IPR001063; Ribosomal_L22.

Pfam; PF00237; Ribosomal_L22; I.

ProDom; PD001032; Ribosomal_L22; I.

ProDem; TIGR01044; rPLV_bact; 1.

TIGRFAMs; TIGR01044; RIBOSOMAL_L22; I.

PROSITE; PS00404; RIBOSOMAL_L22; I.

Ribosomal protein; rRNA-binding; Complete proteome.

Ribosomal protein; rRNA-binding; Gomplete proteome.

SEQUENCE 122 AA; 13048 MW; 63E9285E51901523 CRC64;
                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Q9ZJR8;
Q9ZJR8;
30-MAY-2000
30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99120557; PubMed-9923682; Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doi Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vov
                                                                                                                                                                           EMBL; AE001547;
HSSP; P48286; 1E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic sequence comparison of two unrelated isolates of the gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cleavage
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter.
NCBI_TaxID=85963;
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PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001166; CHH_MIH_GIH.
Pfam; PF01147; Crust_neurohorm; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: THIS PROTEIN BINDS SPECIFICALLY TO 23S IS STIMULATED BY OTHER RIBOSOMAL PROTEINS, E.G., IT IS IMPORTANT DURING THE EARLY STAGES OF 50S RE
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                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
SIMILARITY: BELONGS TO THE L22P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLDA 31
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Similarity 100.0%;
4; Conservative (
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(Rel. 40, Last ann
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26 POTENTIAL.
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a; epsilon subdivision; Helicobacter group;
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BY SIMILARITY.
BY SIMILARITY.
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Pred. No.
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RL22_HELPY
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Best Local S
Matches 4
                                                                                                                                                TIGREAMS; TIGR01044; LPATE PROSITE; PS00464; RIBOSOMAL_L22; 1.

RIBOSOMAL PROSIDE PROSIDE PROSIDE PROTECTION PROSIDE PROTECTION PROSIDE PROTECTION PROBLEMS TO THE PROSIDENCE 122 AA; 13076 MW; C3F02854DFBB7895 CRC SEQUENCE 122 AA; 13076 MW; C3F02854DFBB795 AA; 142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N...

STRAIN=2695 / ATCC 700392;

STRAIN=2695 / ATCC 700392;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

MCKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,

Cotton M.D., Weidman J.M., Fujil C., Bowman C., Watthey L., Wallin E.

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                 Pfam; PF00237; Ribosomal_L22; 1.
ProDom; PD001032; Ribosomal_L22; 1.
TIGRFAMS; TIGR01044; rplv_bact; 1.
                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000633; AAD HSSP; P48286; 1BXE. TIGR; HP1314; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib!ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinf
the European Bioinformatics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 388:539-547(1997).

-i- FUNCTION: THIS PROTEIN BINDS SPECIFICALLY TO 23S RRNA; ITS BITS STIMULATED BY OTHER RIBOSOMAL PROTEINS, E.G., L4, L17, AND IT IS IMPORTANT DURING THE EARLY STAGES OF 50S RECONSTITUTION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001063; Ribosomal_L22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: BELONGS TO THE L22P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori (Campylobacter Bacteria; Proteobacteria; epsilon s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997
16-OCT-2001
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  58
                                                                                                             Local Similarity
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61
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                                                                                            Conservative
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                                                                                                                                    Length 122;
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L outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
A Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
A de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
A de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
A de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
A Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
A Quaggio R.B., Roberto P.G., Santelli R.V., Sawasaki H.E.,
A da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
A da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
A da Silveira J.F., Silvestri M.E., Siqueira W.J., de Souza A.A.,
A da Silveira J.F., Silvestri M.E., Truffi D., Tsai S.M., Tsuhako M.H.,
A de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A zago M.A., Zatz M., Meidanis J., Setubal J.C.;
The genome sequence of the plant pathogen Xylella fastidiosa.";
L. Nature 406:151-159(2000).

C - FERD LAY STITLARTON
                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RS12_XYLFA
Q9PA88;
16-OCT-2001
                                                                                                    TIGREAMS; TIGRO0981; rpst_bact; 1.
PROSITE; PS00055; RIBOSOMAL_S12; 1.
RIBOSOMAL_S12; 1.
RIBOSOMAL_S12; 1.
SEQUENCE 124 AA; 13695 Ma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
                                                                                                                                                                                                           Pfam; PF00164; Ribosomal_S12; 1. PRINTS; PR01034; RIBOSOMALS12. ProDom; PD000576; Ribosomal_S12;
                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                        EMBL; AE004069; AAF85428.1; ALT_INIT. InterPro; IPR000230; Ribosomal_S12.
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                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xylella fastidiosa.
                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STEP (BY SIMILARITY).
SIMILARITY: BELONGS TO THE S12P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 40, (Rel. 40,
                                           Conservative
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                                                          100.0%;
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Last annotation update)
S12.
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                                           0,
                                                             Score 18; I
Pred. No. 2.
                                                                                                                            50211BD3A42C9FD1 CRC64;
                                           Mismatches
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s 0;
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RESULT 24
THN1_WHEAT
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MEDLINE=95125120; PubMed=7824649;

MEDLINE=95125120; PubMed=7824649;

Castagnaro A., Marana C., Carbonero P., Garcia-Olmedo F.;

"CDNA cloning and nucleotide sequences of alpha 1 and alpha thionins from hexaploid wheat endosperm.";

Plant Physiol. 106:1221-1222(1994).
                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Teeter M.M., Max.-Q., Rao U., Whitlow M.;
"Crystal structure of a protein-toxin alpha 1-purothionin a comparison with predicted models.";
Proteins 8:118-132(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohtani S., Okada T., Kagamiyama H., Yosh
"The amino acid sequence of purothionin
to brewer's yeast from wheat.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-78026451; PubMed-914810; Ohtani S., Okada T., Yoshizumi H., Kagamiyama H.; Ohtani S., Okada T., Yoshizumi H., Kagamiyama H.; "Complete primary structures of two subunits of purothionin lethal protein for brewer's yeast from wheat flour."; J. Biochem. 82:753-767(1977).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THI1.1 OR PUR-D1.
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01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Amino acid wheat.";
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[3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 17-61.
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PDB; 2PLH; 03-APR-96.
InterPro; IPR001010;
Pfam; PF00321; plant_
                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91045879; PubMed=2235992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agric. Biol. Chem. 39:2269-2270(1975).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cereal Chem. 54:511-523(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones B.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF THESE PROTEINS IS NOT KNOWN
                                                                                                                                                 A01807;
                                                                                                                                                                                                X70666; CAA50004.1;
                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
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onin A, a lethal toxic
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RESULT 25
UL33_HSV11
AC P10217;
D7 01-MAR-1989
D7 01-DEC-1992
D8 Protein UL3:
GN UL33.
GN UL33.
GN UL33.
GN Herpes simploc Viruses; dsf UL3:
GN UL33.
OS Herpes simploc NCBI_TaxID=1
RN [1]
RP SEQUENCE FR(RX MEDLINE-882;
RA MCNAD D., PR MCRAD D., PR MCRA
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Matches 4
                                                                                                                                                                                                 EMBL; D10879; BAA01679.1; --
EMBL; X14112; CAA32308.1; --
EMBL; M62932; AAA45829.1; --
                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-MAR-1989 (Rel. 1
01-DEC-1992 (Rel. 1
                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VITOLOGY 180:380-388(1991).
-!- FUNCTION: STRUCTURAL; INVOLVED
-!- SIMILARITY: BELONGS TO FAMILY 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91082431; PubMed=1845831;
Al-Kobaisi M.F., Rixon F.J., McDougall I., Preston V.G.;
"The herpes simplex virus UL33 gene product is required assembly of full capsids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C., McNab D., Perry L.J., Scott J.B., Taylor P.;
"The complete DNA sequence of the long unique region in the genome herpes simplex virus type 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988)
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NCBI_TaxID=10299;
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                                                                                                                                          PF03581;
             4.
                                  Similarity
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                                                                                                                                                      IPR005208; Herpes_UL33.
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                                                                                                 130 AA;
         Conservative
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10, Last sequence update)
24, Last annotation update)
                                                                                           14437 MW;
                           100.0%;
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41
13525 MW;
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         0;
    Score 18; DE
Pred. No. 2.7
0; Mismatches
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Pred. No. 2.6
); Mismatches
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                                                                                        >D: TEMPERATURE SENSITIVE.
D04CFDA7A3C585D3 CRC64;
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F GROUPS TOGETHER HSV-1 UL33,
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                                               DB 1;
                         .7e+02;
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                                           Length 130;
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Gaps
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RESULT 27
SFP1_BOVIN
ID SFP1_B
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YY08_MYCTU
YY08_T7717;
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        SFP1_BOVIN
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Hypothetical protein; Complete proteome.
CONFLICT 43 43 S -> L (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 277165; CAB01015.1; ALT_INIT.
EMBL; AE007157; AAK47854.1; -
TIGR; MT3516; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CDC 1551 / Oshkosh;
FleisChmann R.D., Alland D., Elsen J.A., Carpenter L., White O Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzbe Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Miku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C., III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Chillingworth T., Connor R., Chillingworth T., Gentles S., Squares T., Rutter S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.", Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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Q50717;
Q1-NOV-1997 (Rel. 35, Created)
116-OCT-2001 (Rel. 40, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
115-JUN-2002 (Rel. 41, Last annotation update)
115-JUN-2002 (Rel. 41, Last annotation update)
115-JUN-2002 (Rel. 40, Last sequence update)
116-OCT-2001 (Rel. 35, Created)
116-OCT-2001 (Rel. 35, Created)
116-OCT-2002 (Rel. 35, Created)
116-OCT-2001 (Rel. 35, Created)
116-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whole genome comparison of Mycobacterium tuberculosis
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     STANDARD;
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  PRT;
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01-AUG-1991 (Rel. 19, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Seminal plasma protein PDC-109 precursor (Sem
protein 109) (SVSP109) (BSP-Al and BSP-A2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                           Constantine K.L.,
                                                                                                                                                                                                 STRUCTURE BY NMR OF MEDLINE=92114067; Pu
                                                                                                                                                                                                                                                                          Biochemistry
                                                                                                                                                                                                                                                                                                "Sequence-specific of bovine seminal
                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 95-134.
MEDLINE-91129241; PubMed-1993183;
Constantine K.L., Ramesh V., Bany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerwig G.L., Calvete J.J., Toepfer-Petersen E., Vliegenthart J.F.G.; "The structure of the O-linked carbohydrate chain of bovine seminal plasma protein PDC-109 revised by H-NMR spectroscopy A correction."; FEBS Lett. 387:99-100(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE OF CARBOHYDRATE ON THR-36. MEDLINE-96234019; PubMed-8654577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spermatozoa.";
FEBS Lett. 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seminal plasma and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYDRATE-LINKAGE SITE THR-36.
MEDLINE-94350099; PubMed-8070564;
Calvete J.J. Raida M., Sanz L., Wempe F.,
Toepfer-Petersen E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83256590; PubMed-6870895;
Esch F.S., Ling N.C., Boehlen P., Ying S.Y., Guillemin R.;
"Primary structure of PDC-109, a major protein constituent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Braeuer C.C., Kleine
Submitted (MAY-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of the gene for the bovine secretory protein SVSP109.";
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                                                                                                        domain b.
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                                                                                                                                                                                                                                                                                                                                               Llinas M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Localization and structural characterization of an oligosaccharide

)-linked to bovine PDC-109. Quantitation of the glycoprotein in

seminal plasma and on the surface of ejaculated and capacitated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Cloning
                                                                                                                                 Refined
ain b. A collagen-binding type II domain.";

wol. Biol. 223:281-298(1992).

FUNCTION: COULD ENHANCE THE FERTILIZING CAPACITY OF BULL

SPERMATOZOA UPON INTERACTION WITH HEPARIN-LIKE GLYCOSAMINOGLYCANS

PRESENT IN THE FEMALE GENITAL TRACT. EXHIBITS BOTH SIMULATORY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7:595-599(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Scheit K.H.; and sequence analysis of a the precursor of the major
                                                                                                   solution structure and ligand-binding. A collagen-binding type II domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biophys.
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                                                                                                                                                                                                                                                                     scific 1H NMR assignments and structural characterization
ninal fluid protein PDC-109 domain b.";
30:1663-1672(1991).
                                                                                                                                                                           OF 95-134.
PubMed=1731074;
Madrid M., Bany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Res. Commun. 113:861-867(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=1932121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=3229283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuhlmann J.J., Hanes J.J., Scheit to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                         Banyai L.,
                                                                                                                                                                                                                                                                                                                                                                   Banyai L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA from seminal vesicle protein of bull semen.";
                                                                                                                                                                           Trexler M.,
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                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000562; FN_Type_II.
Pfam; PF00040; fn2; 2.
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PIR; S18404;
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- SIMILARITY: (
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L; X60495; CAA43021.1; -.
L; X60496; CAA43021.1; JOINED.
L; X60497; CAA43021.1; JOINED.
L; X60498; CAA43021.1; JOINED.
L; X60969; -; NOT_ANNOTATED_CDS
L; X60960; -; NOT_ANNOTATED_CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INHIBITORY ACTIONS ON THE RELEASE OF PITUITARY GONADOTRO SUBUNIT: HOMODIMER.
TISSUE SPECIFICITY: MAJOR COMPONENT OF SEMINAL PLASMA.
PTM: O-GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH MODIFIED WITH A SIALIC ACID RESIDUE (MACRO-AND/OR MICROHETEROGENEITY ACCOUNT FOR DIFFERENCES BETWEEN BSP-A
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/FTId=CAR_000071.
                                     0;
                                     Score 18; DE Pred. No. 2.8); Mismatches
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RESULT 28
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RESULT 29
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ID YNPO_Y
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Hypothetical 14.8 k
YNL150W OR N1773
                                         Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycesaccharomycetales; Saccharomycetaceae; Sa
 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00332; HISTRIAD.
PROSITE; PS00892; HIT; 1.
Hypothetical protein; Complete
SEQUENCE 134 AA; 14712 MW;
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EMBL; Z95151; CAB08415.1; -.
EMBL; AL583924; CAC31193.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-1- SIMILARITY: BELONGS TO THE HIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P80912; 4RHN.
Leproma; ML2237; -.
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Barrell B.G.;
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                                                                                                                                                                                                                                                                                 118 SLDA 121
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Smith D.R., Robison K.;
Submitted (SEP-1994) to
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Hypothetical HIT-like p
ML2237 OR MLCB5.04C OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
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NCBI_TaxID=1769;
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                                                                                                                                                                                               STANDARD;
                                                                                                                              . 34, Created)
. 34, Last sequ
. 36, Last anno
                                       Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                            Score 18;
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C1853F3ADF7239A7 CRC64;
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RPC8-MFA2 intergenic region
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RESULT 30
THN2_WHEAT
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Best Local
                                TISSUE-Endosperm;

MEDLINE-95125120; PubMed-7824649;

Castagnaro A., Marana C., Carbonero P., Garcia-Olmedo F.;

Castagnaro A., Marana C., Carbonero P., Garcia-Olmedo F.;

CONA cloning and nucleotide sequences of alpha 1 and alpha 2

thionins from hexaploid wheat endosperm.";

Plant Physiol. 106:1221-1222(1994),

-1- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC

TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE

LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,

OF THESE PROTEINS IS NOT KNOWN.

-1- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
                    This
                                                                                                                                                                                                                                                         Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Stra
Spermatophyta; Magnoliophyta;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                               Alpha-2-purothionin
THI1.2 OR PUR-B1.
                                                                                                                                                                                                                                                                                                                                      01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence up
01-NOV-1995 (Rel. 32, Last annotation
                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                           NCBI_TaxID=4565,
                                                                                                                                                                                                                                                                                                                                                                                         P32032;
                                                                                                                                                                                                                                                                                                                                                                                                          THN2_WHEAT
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DOMAIN 41 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; x92517; CAA63289.1; -. EMBL; Z71424; CAA96032.1; -. EMBL; Z71426; CAA96036.1; -. SGD; S0005094; YNL150W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mallet L., Bussereau F., Jacquet M.;
"A 43.5 kb segment of yeast chromosome XIV, which contains MEP2, CAP/SRV2, NAM9, FKB1/FPR1/RBP1, MOM22 and CPT1, prediadenosine deaminase gene and 14 new open reading frames."; Yeast 11:1195-1209(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 SLDA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288c / FY1679;
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SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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yta; Liliopsida;
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; 22EC1EC99F3DDD45 CRC64;
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a; Poales; Poaceae; Pooideae;
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Thionin;
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Ohtani S.
                                                                                                                                                                                                                                                                                                               STRAIN-cv. Manitoba 3;
MEDLINE-78026451; PubMed-914810;
Ohtani S., Okada T., Yoshizumi H., Kaga
"Complete primary structures of two sub-
lethal protein for brewer's yeast from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986
15-JUL-1998
15-JUL-1998
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"The amino acid sequence
to brewer's yeast from wh
Agric. Biol. Chem. 39:226
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Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Triticeae; Triticum.
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                                                           "The amino acid sequence of wheat Can. J. Biochem. 54:835-842(1976).
                                                                                               SEQUENCE OF 28-72.
MEDLINE-77046666; Pub
Mak A.S., Jones B.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 28-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Rosella;
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                    X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS)
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                                                                                                                                                                                                                                                                                               thal protein for brewer's yeast Biochem. 82:753-767(1977).
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|| SLDA 136
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(Rel. 36,
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    Teeter M.M.;
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a; Poales; Poaceae; Pooideae;
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STRAIN-Bristol N2;
Bradshaw-Cordum H., Scott K., Graves T.;
Bradshaw-Cordum H., Scott K
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Acta Crystallogr. D 51:914-924(1995).
-I- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; renverse; plant_thionins; pfam; pF00321; plant_thionins; pr00328; TOXIN.

PROSITE; pS00271; THIONIN; 1.

Thionin; Plant toxin; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF004018; AAB71137.1; -. PIR; A01806; VSWTA1.
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                                                                                                                                                                                                                                                                                                                                                                                         Black B.E., Levesque L., Holaska J.M
"Identification of an NTF2-related f
regulates nuclear protein export.";
Mol. Cell. Biol. 19:8616-8624(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9U757;
16-OCT-2001
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InterPro; IPR001219;
InterPro; IPR001010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-20036817; PubMed-10567585;
Black B.E., Levesque L., Holaska J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTF2-related export protein. NXT1 OR Y71F9AM.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhabditidae; Pel
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
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15-JUN-2002
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
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Pred. No. 2.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.M., Wood T.C., Paschal B.M.; ed factor that binds Ran-GTP an
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MEDLIND-21470413; PubMed-11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

"Genome sequence of Versinia pestis, the causative agent of plague."

"Astrona A.1. 2021-2770001
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                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Eucopean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
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78ZC42;
75-JUN-2002 (Rel. 41, Createg)
75-JUN-2002 (Rel. 41, Last sequence update)
75-JUN-2002 (Rel. 41, Last annotation update)
75-JUN-2002 (Rel. 41, Last annotation update)
75-JUN-2002 (Rel. 41, Last annotation update)
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WormPep; Y71F9AM.5; CE26780.
Interpro; IPR002075; NTF2.
Pfam; PF02136; NTF2; 1.
PROSITE; PS50177; NTF2_DOMAIN; 1.
Transport; Protein transport; mRNA transport; Nuclear protein.
DOMAIN
19 135 NTF2_COMAIN; 1.
                                                                               EMBL; AJ414155; CAC92416.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
-!- SIMILARITY:
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HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Involved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
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Pro; IPR000139; PF01029; NusB:
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an email to license@isb-sib.ch).
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Pred. No. 2.8e+02;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    process (By
                                                                                                                                                                                                                                                                                                                                                 gh a collaboration EMBL outstation
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Best Local Similarity
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                                                                                                                HFAA_CAUCR STANDARD;

P27342; 068957;

01-AUG-1992 (Rel. 23, Created

16-OCT-2001 (Rel. 40, Last sec

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HOLdfast attachment protein A

HFAA OR CC2628
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                                               Caulobacter
                                                                   Bacteria; Proteobacteria; alpha subdivision; Caulobacter group
                                                                                               Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dutreix M., Baeckman A., Celerier J., Bagdasarian m.m., Summer S., Bailone A., Devoret R., Bagdasarian M.;
"Identification of psiB genes of plasmids F and R6-5. Molecular basis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE-89083490; PubMed=3205720; |

MEDLINE-89083490; PubMed=3205720; |

MEDLINE-80083490; PubMed=80083490; |

MEDLINE-80
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Nucleic Acids Res. 16:10669-10679(1988).
-I- FUNCTION: INHIBITION OF THE INDUCTION OF THE SOS PATHWAY.
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PSIB.
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SEQUENCE 138 AA; 15506 MW;
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Pred. No.
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Best Local Similarity
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RS12_SULSO
P39573;
01-FEB-1995
16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nierman W.C., Feidblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-ATCC 19089 / CB15;
MEDLINE-21173698; PubMed=11259647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 19089 / CB15;
MEDLINE-99138730; PubMed-9973336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kurtz H.D. Jr., Smit J.;

"Analysis of a Caulobacter crescentus gene cluster involved attachment of the holdfast to the cell.";

J. Bacteriol. 174:687-694(1992).
           16-OCT-2001 (Rel. 40, Last annotation update) 30S ribosomal protein S12P. RPS12P OR RPS12 OR RPS12AB OR SSO0219.
                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF058792; AAC14298.1; EMBL; AE005930; AAK24596.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
-i- FUNCTION: INVOLVED IN ATTACHMENT OF THE HOLDFAST TO THE CELL.
HOLDFAST IS A STRUCTURE THAT ALLOWS THE BACTERIA TO FIRMLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 181:1118-1125(1999)
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S.MARCESCENS SMFG C-TERMINI.
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G -> R (I
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S -> N (IN REF. 2).
NSSQV -> IQDGE (IN REF. 1).
09B10FE5DFDE436F CRC64;
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Pred. No.
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Q976A8;
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15-JUN-2002
15-JUN-2002
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"The complete genome of the crenarchaeon Sulfolobus solfataricus P2. Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                          Sulfolobus tokodaii.
Archaea; Crenarchaeota;
                                                                 RPS12P OR ST0272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE006659; AAK40562.1; ALT_INIT.
InterPro; IPR000230; Ribosomal_S12.
Pfam; PF00164; Ribosomal_S12; 1.
ProDom; PD000576; Ribosomal_S12; 1.
TIGRFAMS; TIGR00982; S23_S12_E_A; 1.
PROSITE; PS00055; RIBOSOMAL_S12; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21332296; PubMed=11427726;
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Arcari P., Gallo M., Ianniciello G.,
"The nucleotide sequence of the green"The nucleotide sequence of the green of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; Complete proteome.
                                                                            (Rel. 41, Crearce, Property of Rel. 41, Last sequence up 2 (Rel. 41, Last annotation and protein S12P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \begin{array}{c} 128 \\ 147 \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; ilarity 100.0%; Conservative 0;
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                                                                                                                                                                                                                             STANDARD;
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129
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                       Thermoprotei; Sulfolobales;
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P -> S (IN STRAIN N
A -> S (IN STRAIN N
D -> N (IN STRAIN N
D -> NG (IN REF. 1
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Pred. No. 3.1e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 -> NG (IN REF. 1).
740BFFB1849BDE32 CRC64;
                                                                                                                         on update)
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MT-4).
MT-4).
MT-4).
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                          Sulfolobaceae;
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RESULT 38
TPCB_HOMAM
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"Lobster troponin C: amino acid sequences of three isoforms.";
Arch. Biochem. Biophys. 291:89-91(1991).
-!- FUNCTION: TROPONIN IS THE CENTRAL REGULATORY PROTEIN OF STRIATED MUSCLE CONTRACTION. TN CONSISTS OF THREE COMPONENTS: TN-I WHICH IS THE INHIBITOR OF ACTOMYOSIN ATPASE, TN-T WHICH CONTAINS THE BINDING SITE FOR TROPOMYOSIN AND TN-C. THE BINDING OF CALCIUM TO TN-C ABOLISHES THE INHIBITORY ACTION OF TN ON ACTIN FILAMENTS.
-!- MISCELLANEOUS: THERE ARE THREE DIFFERENT TROPONIN C IN LOBSTER.
-!- MISCELLANEOUS: THIS PROTEIN BINDS TWO CALCIUM FONS.
                                                                                                                                                                                                                                                                                                                                         TISSUE-Abdominal flexor muscle;
MEDLINE-92027802; PubMed-1929438;
Garone L., Thelbert J.L., Miegel A.,
                                                                                                                                                                                                                                                                                                                   Collins J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa: Arthropoda; Mandibulata; Pancrustacea; Crustacea; Malacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea; Nephropoidea; Nephropoidae; Homarus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IFR000230; Ribosomal_S12.
Pfam; PF00164; Ribosomal_S12; 1.
ProDom; PD000576; Ribosomal_S12; 1.
TIGRFAMS; TIGR00982; S23_S12_E_A; 1.
PROSITE; PS00055; RIBOSOMAL_S12; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/orsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homarus americanus (American lobster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7."; DNA Res. 8:123-140(2001).
-I-FUNCTION: Protein S12 is involved in the translation initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribosomal protein; Complete proteome. SEQUENCE 147 AA; 16336 MW; 5BC87E
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MEDLINE=21456156; PubMed=11572479;
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SIMILARITY: BELONGS TO THE S12P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
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Pred. No. 3.
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s 0;
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RESULT 39
MRAZ_PSEAE
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                                                      TIGREAMS;
Complete p
SEQUENCE
                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                         EMBL; AE004856; AAG07809.1; -. InterPro; IPR003444; UPF0040.
                                                                                                                                                                                                                                                     "Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406:959-964(2000).
-!- SIMILARITY: BELONGS TO THE MRAZ FAMILY.
                                                                                                                                                                                                                                                                                                      MEDLINE-20437337; PubMed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9HVZ4;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                Pfam; PF02381; UPF0040;
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA_BIND
SEQUENCE
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CA_BIND
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MRAZ OR PA4421.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRAZ_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00036; efhand; 4. ProDom; PD000012; EF-hand; 2. SMART; SM00054; EFh; 4.
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Muscle protein; Calcium-binding; Repeat;
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HSSP: P02588; lAVS.
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3 SLDA 6
                Similarity
                                                      proteome.
151 AA;
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                                                                                  TIGR00242;
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     Conservative
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67 E
107 A
143 E
; 16951 MW;
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               100.0%;
                                                                                  TIGR00242;
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    0;
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ACETYLATION (BY SIMILARITY).
ANCESTRAL CALCIUM SITE 1 (POT
EF-HAND 2 (PROBABLE).
ANCESTRAL CALCIUM SITE 3 (POT
EF-HAND 4 (PROBABLE).
EF-HAND 5 (PROBABLE).
EF-HAND 5 (PROBABLE).
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            Score 18; DB 1;
Pred. No. 3.2e+02;
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  Mismatches
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P55518;
01-NOV-1997
01-NOV-1997
15-JUN-2002
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"Organization and nucleotide sequence of the
subunits A, B and C of the DNA-dependent RNA
archaebacterium Sulfolobus acidocaldarius.";
Nucleic Acids Res. 17:4517-4534(1989).
-I- FUNCTION: PROTEIN S12 IS INVOLVED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1989
01-NOV-1995
30-MAY-2000
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P11524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                          RHISN
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                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000576; Ribosomal_S12; 1. TIGRFAMS; TIGR00982; S23_S12_E_A; 1. PROSITE; PS00055; RIBOSOMAL_S12; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sulfolobus acidocaldarius
 SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
                                                   Rhizobiaceae;
                                                              Plasmid sym pNGR234a.
Bacteria; Proteobacteria;
                                                                                       Rhizobium sp.
                                                                                                                Hypothetical
                                                                                                                                                                                                                                            133
                                                                                                                                                                                                                                                                                                                                                       Ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X14818; CAA32929.1; ALT_INIT.
PIR; S04721; R3UC12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPS12P OR RPS12
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00164; Ribosomal_
                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                   1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE S12P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                                                                                           SLDA 136
                                                                                                                                                                                                                                                                                            4.
                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000230; Ribosomal_S12.
                                                                                                               (Rel. 35,
(Rel. 35,
(Rel. 41,
11 17.3 kDa
                                                                                                                                                                                                                                                                                                                                           151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel.
                                                                                                                                                                                                                                                                                            Conservative
                                                   Rhizobium.
                                                                                       (strain NGR234).
                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32,
                                                                                                                                                                                                                                                                                                                                           16570 MW;
                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last annotation S12P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                protein
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                                                              alpha
                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                    Score 18; DB 1;
Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                           3867AE02D161491F CRC64;
                                                                                                                                                                                                                                                                                          Mismatches
                                                               subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                             151 AA
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                                                               Rhizobiaceae
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                                                                                                                                                                                                                                                                                                                  Length 151;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                          Gaps
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RESULT 42
COBE_PSEDE
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Best Local :
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01-MAY-1991
01-JUL-1993
                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Experimental Conformatics Institute. There are no restructed by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.lsb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                    Crouzet J., Cauchois L., Blanche F., Debussche L., Thibaut D., Rouyez M.-C., Rigault S., Mayaux J.-F., Cameron B.; "Nucleotide sequence of a Pseudomonas denitrificans 5.4-kilobase DNI fragment containing five cob genes and identification of structural genes encoding S-adenosyl-L-methionine: uroporphyrinogen III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular basis of symbiosis between Rhizobium and legumes."; Nature 387:394-401(1997).
-!- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
                                                                                              entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 151 AA;
                                                                                                                                                                                                                                         methyltransferase and cobyrinic acid a,c-diamide synthase J. Bacteriol. 172:5968-5979(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CobE protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COBE_PSEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; DOMAIN 1 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
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SMART; SM00448; REC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Freiberg C.A.,
                                                                                                                                                                                                                                                                                                                                            MEDLINE-91008975; PubMed-2211520;
                                                                                                                                                                                                                                                                                                                                                             STRAIN-SC510;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=43306;
                                                                                                                                                                                                                                                                                                                                                                                                                   seudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                eudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000080; AAB91730.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 SLDA 115
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                                                                                                                                                                                                               TO COBYRINIC ACID.
                                                                                                                                                                                                                           PATHWAY: COBALAMIN BIOSYNTHESIS; TRANSFORMATION OF PRECORRIN-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteobacteria;
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(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                              denitrificans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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. 18, Last sequ
. 26, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESPONSE REGULATORY.
F8B42BCF7845E03F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 1;
Pred. No. 3.2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                 subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                It is produced through a control of the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions
                                                                                                            http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                      restrictions
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                                                                                                                                                                     EMBL outstation
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                                                                                                                                                                                 a collaboration
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EMBL; M59236; AAA25772.1; -. PIR; A36144; A36144.

Pfam;

[nterPro;

Pro; IPR002750; PF01890; CbiG;

cbiG.

biosynthesis; Porphyrin biosynthesis.
154 AA; 15487 MW; 197D77DC4CE20BAE CRC64;

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RESULT 43
VATL_HELVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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Best Local
     BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                   This SWI
between
                                                                                                                                                                                           EMBL; L16884; AAC37176.1; -.
InterPro; IPR002379; ATPase_Csub.
InterPro; IPR000245; Vac_ATPsynt_Csub.
Pfam; PF00137; ATP-synt_C; 2.
                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996
01-OCT-1996
15-JUN-2002
                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                              modified and this entities requires
                                                                                                                                                                                                                                                                                                           use
                                                                                                TRANSMEM
                                                                                                                           TRANSMEM
                                  DOMAIN
                                                           DOMAIN
                                                                      TRANSMEM
                                                                                      DOMAIN
                                                                                                                 DOMAIN
                                                                                                                                                      Hydrolase;
                                              TRANSMEM
                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pietrantonio P.V., Gill S.S.;
"Sequence of a 17 kDa vacuolar H(+)-ATPase proteolipid subunit from insect midgut and Malpighian tubules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ditrysia; Noctuc
NCBI_TaxID=7102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heliothis virescens (Noctuid moth)
Eukaryota; Metazoa; Arthropoda; Mar
Insecta; Pterygota; Neoptera; Endor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vacuolar ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VATL_HELVI
P55277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insect Biochem. Mol. Biol. 23:675-680(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93357792; PubMed=8353524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                  AS A HEXAMER THAT FORMS THE PROTON-CONDUCTING PORE).
SUBCELLAULAR LOCATION: Integral membrane protein. Vacuolar MISCELLANDEOUS: THIS SUBUNIT BINDS DICYCLOHEXYLCARBODIIMIDE (DCI WHICH INHIBITS THE ATPASE (BY SIMILARITY).
SIMILARITY: BELONGS TO THE V-ATPASE PROTEOLIPID SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                   H(+)(Out).

SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON POR COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN; WHICH IS PROTECTED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: PROTON-CONDUCTING PORE FORMING SUBUNIT OF THE MEMBRANE INTEGRAL VO COMPLEX OF VACUOLAR ATPASE. V-ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOR ACIDIFYING A VARIETY EUKARYOTIC CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLDA 58
                                                                                                                                                                                  PR00122;
                                                                                                                                                                                                                                                                                        non-profit institutions as long and this statement is not removed.
                                                                                                                                          TIGRO1100; V_ATP_synt_C; 1.
Hydrogen ion transport; ATP synthesis; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Metazoa; Arthropoda; Mandibulata; i
Pterygota; Neoptera; Endopterygota; i
Noctuoidea; Noctuidae; Heliothinae;
                               31
31
53
74
74
115
115
115
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nilarity 100.
Conservative
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
P synthase 16 kDa proteolipid subu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                               VACATPASE
                               30
52
73
92
114
126
152
     15934
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     MW.
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DICYCLOHEXYLCARBODIIMIDE; E8DB1065B896E4B5 CRC64;
                                                    POTENTIAL.
CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                          POTENTIAL.
                             LUMENAL (POTENTIAL).
                                                                               LUMENAL (POTENTIAL).
                                                                                            POTENTIAL
                                                                                                           CYTOPLASMIC
                                                                                                                           POTENTIAL
                                                                                                                                      LUMENAL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156
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                                                    (POTENTIAL).
                                                                                                          (POTENTIAL).
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                                                                                                                                                                                                                                                                                        Usage
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; Heliothis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pancrustacea;
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            (POTENTIAL).
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2.f)
(Lumazine synthase) (Riboflavin synthase beta
                                                                                                                RISB_MYCTU
P71685;
01-NOV-1997
16-OCT-2001
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P16792;
01-AUG-1990
01-AUG-1990
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A
                       NCBI_TaxID=1773;
                                   Actinomycetales;
                                                    Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF03581; Herpes_UL33;
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X17403; CAA35410.1; -. PIR; S09814; S09814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., B "Analysis of the protein-coding content of the sequence cytomegalovirus strain AD169.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Breddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                         Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=90269039; PubMed=2161319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical UL51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _HCMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Betaherpesvirinae; Cytomegalovirus; NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR005208; Herpes_UL33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UL51_HCMVA
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157 AA:
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(Rel. 15, Last sequence up
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                                                                                                                                                                     STANDARD;
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                                    Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                            16968 MW;
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cterineae; Mycobacteriaceae;
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Pred: No. 3.3e+02;
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                                               Actinobacteridae;
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REMBL; AE007016; AAK45724.1; -.

RHSSP; O66529; HUK.

RTIGR; MT1459; -.

RTIGR; MT1459; -.

RIGHEPTO; IPR002180; DMRL_synthase.

Pfam; PF00885; DMRL_synthase; 1.

PFADOM: PD003664; DMRL_synthase; 1.

RPTODOM: PD003664; DMRL_synthase; 1.

RTIGREAMS; TIGR00114; ribH; 1.

RTIGREAMS; TIGR00114; ribH; 1.

RTIGREAMS; TIGR00114; ribH; 1.

RTIGREAMS; TIGR00114; ribH; 1.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

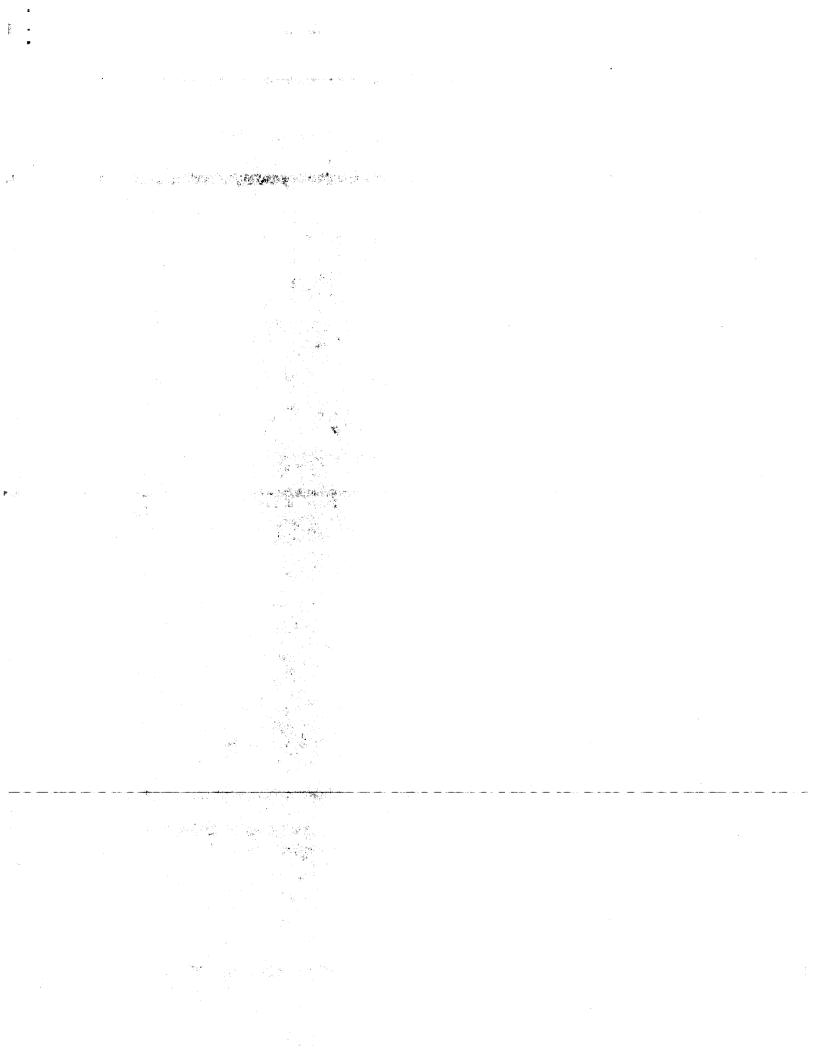
-!-FUNCTION: Riboflavin synthase is a bifunctional enzyme complex catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By similarity).

-!-CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-lumazine (By similarity).

-!-CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-p-ribityl)lumazine - riboflavin + 4-(1-p-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.

-!- SIMILARITY: BELONGS TO THE DMRL SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CDC 1551 / Oshkosh;
FleisChmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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nes 4; Conserv
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Search completed: February 6, 2003, 11:16:48 Job time: 7.33333 secs



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Q9z775 chlamydia p
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ALIGNMENTS

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Q1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                            Chistoserdova L., Lidstrom M.;
"Cloning of a hydroxypyruvate reductase gene from Methylextorquens AM1, mutagenesis of the gene.";
Submitted (CCT-1991) to the EMBL/GenBank/DDBJ databases
EMBL; M74226; AAA25377.1; -.
Q8X4F2;
01-MAR-2002 (TrEMBLrel. 20,
                          Q8X4F2
                                                                                                                                                                                                     Oxidoreductase; Pyruvate. NON_TER 20 20
                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=408;
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SEQUENCE FROM N.A.
Andreoni F., Ruzzo A., Magnani M.;
Andreoni For sequence variation in
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Bovidae; |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
Nature 409:529-533(2001).
EMBL; AE005559; ARG59475.1; -
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Bacteria; Proteobacteria;
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MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                          Local
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AF309638; AAL87545.
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Eutheria; Cetartiodactyla; Ruminantia; Pecora;
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                            PRELIMINARY;
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4074 MW;
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Pred. No. 4.1
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Pred. No.
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RESULT Q947911 ID 20 AC Q9 AC Q9 DT 
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Best Local
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Q94791;
01-FEB-1997 (TREMBLICAL 0
01-FEB-1997 (TREMBLICAL 0
01-MAR-2002 (TREMBLICAL 2
                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97026280; Pui
Ben-Arie N., McCall &
Zoghbi H.Y.;
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Eukaryota;
Pterygota;
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01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
101-MAR-2002 (TrEMBLrel. 2
Hypothetical protein z118
Z1184 OR z1623
                                                                                                                                                                                                                                                                            "Evolutionary conservation of sequence and expression of protein Atonal suggests a conserved role in neurogenesis. Hum. Mol. Genet. 5:1207-1216(1996).
EMBL; U61152; AAB&1307.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.", Nature 409:529-533(2001), EMBL; AE005311; AAG55378.1; -EMBL; AE005274; AAG55379.1; -EMBL; AE005274; AAG55379.1; -IPPOthetical protein; Complete proteome.
                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                          SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tribolium castaneum (Red floue Eukaryota; Metazoa; Arthropoce Pterygota; Neoptera; Endoptes Cucujiformia; Tenebrionidae;
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Pfam; PFO0010;
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STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
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26
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29
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Arthropoda; Tracheata; Hexapoda; Insecta;
; Endopterygota; Coleoptera; Polyphaga;
rionidae; Tribolium.
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Pred. No. 4.9
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Q8SPU2;
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
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Q941Y6;
Q1-DEC-2001
01-DEC-2001
01-DEC-2001
01-JUN-2002
P0431G06.24
P0431G06.24
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Q9NMC6;
01-OCT-2000
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Murphy L., Quail M., Harris
Submitted (JUL-2000) to the
EMBL; AL160493; CAB97784.1;
NON_TER 51 51
                                                                                                                                                                                                                                                                                        Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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01-OCT-2000
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NCBI_TaxID=9544;
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        (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
protein (Bil39B11.2 protein).
OR Bil39B11.2.
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(TrEMBLrel. 15, Last sequence up)
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(Rice),
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Q8YL68;
Q1-MAR-2002
01-MAR-2002
01-MAR-2002
                                                                        Plasmid;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica.cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID-4530, 39947;
[1]
                                                                                       "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
EMBL; AP003600; BAB78151.1;
                                                                                                                                                                                                               Anabaena sp. (strain PCC 7120).
Plasmid pCC7120alpha.
Bacteria; Cyanobacteria; Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOY-2001) to the EMBL; AP003683; BAB64712.1; EMBL; AP004368; BAB90774.1; SEQUENCE 52 AA; 6048 MW;
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STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yaman
"Oryza sativa nipponbare(GA3)
clone:B1139B11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
                                                                                                                                                                                                                                            Hypothetical protein ASR7067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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Hypothetical protein; Complete proteome.
53 AA; 5639 MW; 3D75D4AA82284175 CRC
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hes 0;
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Yersinia pestis.

Bacteria; Pro+-
Yersinia, Pro+-
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Q9Z775;
01-MAY-1999
01-MAY-1999
                                                                                                                                             "Genomic sequence comparison of pneumoniae from Japan and U.S."; Submitted (JAN-2000) to the EMBL
                                                                                                                                                                                                                                              STRAIN-J138;
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., Lammel C. Olinger L., Grimwood J., Davis R.W., Stephens "Comparative genomes of Chlamydia pneumoniae Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein CPn0831
CPN0831 OR CPJ0831 OR CPJ0839.
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EMBL; Au414148 CAC90253.1; -.

Hypothetical protein; Complete proteome.

55 AA; 6406 MM; B7CE6B7FEFDAD6E2 CRC64;
                                          MEDLINE=20150255; PubMed=10684935; Read T.D., Brunham R.C., Shen C.,
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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MEDLINE-21470413; PubMed-11586360;
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Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F.
Shiba T., Ishi K., Hattori M., Kuhara S., Nakazawa T.,
Shiba T., Ishi K., Hattori M., Kuhara S., Nakazawa T.,
Comparison of whole genome sequences of Chiamydia pneu from Japan and CWL029 from USA.";
L Nucleic Acids Res. 28:2311-2314(2000).
R EMBL; AE001663; AAD18968.1; -.
R EMBL; AE002541; BAA88649.1; -.
R EMBL; AE002541; BAA88649.1; -.
R EMBL; AE002541; BAA888649.1; -.
R EMBL; AE002541; BAA88849.1; -.
R EMBL; AE002541; BA
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Q9K1Z5;
01-OCT-2000
01-OCT-2000
01-OCT-2001
  Q9ZI54
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Nucleic Acids Res. 28:1397-140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20150255; PubMed=10684935; | Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hokey E.K., Peterson J., Utterback T., Berry K., Butte C., Hokey E.K., Khouri H., Craven B., Bowman C., Dodson Gwinn M., Weidman J., Khouri H., Craven B., McClarty G., Salzb
                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 62 AA; 6840 MW;
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Eisen J., Fraser C.M
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Bacteria; Chlamydiales;
NCBI_TaxID=83558;
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Nelson W., DeBoy R., Kolonay
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) (TremBLrel. 15, () (TremBLrel. 15, I) (TremBLrel. 18, I) (TremBLrel. 18, I) al protein CP0758.
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  PRELIMINARY;
                                                                                                                                                                                                                                                         Conservative
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llarity 100.0%;
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6 AA; 6344 MW; 0:
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AAF38560.1; -.
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Chlamydiaceae; Chlamydor
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Pred. No. 6.2
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057543635D28B661 CRC64;
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63
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Salzberg S.L.,
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01-MAY-1999
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O9Z431 PRELIMINARY; PRT;
O9Z431;
O1-MAY-1999 (TYEMBLTel. 10, Created)
O1-MAY-1999 (TYEMBLTEL 10, Last seq
O1-JUN-2002 (TYEMBLTEL 21, Last ann
                                                                                                                                                                                                                                                               EMBL; AF100302; AAD13221.1;
HSSP; P49172; 10TF.
                                                                                                                                                                                                                                                                                                           Grimm A.C., Harwood C.S.;

Nahy, a catabolic plasmid-encoded Pseudomonas putida to the aromatic J. Bacteriol. 181:3310-3316(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4-oxalocrotonate
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Pfam; PP01361; Tautomerase; 1.
ProDom; PD019232; Tautomerase;
TIGRFAMs; TIGR00013; taut; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas štutzeri AN10.";
Gene 245:65-74(2000).
EMBL; AF039534; AA002155.1;
HSSP; Q01468; IBJP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bosch R., Garcia-Valdes E., Moore E.R.B.;
"Complete nucleotide sequence and evolutionary significance chromosomally encoded naphthalene-degradation lower pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                              InterPro; IPRO04370; Taut.
Pfam; PF01361; Tautomerase; 1.
ProDom; PD019232; Tautomerase;
TIGRFAMs; TIGRO0013; taut; 1.
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                                                                                                                                                           Plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99255564; PubMed-10322041;
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                                            Local Similarity
nes 4; Conserv
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                                                                                                                                    7122 MW;
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                                                                 100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                receptor required for chemotaxis of
hydrocarbon naphthalene.";
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                                                                   7e+02;
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                                              Indels
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Best Local S
Matches 4
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Best Local (
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Q9R9T3;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2002
                                                                                                                                                                                                                   Baker R.F., Azadpour E.E., Luo X., Benjamin R.C., "Sequence of the lower (meta-cleavage) xyl operon putida TOL plasmid pDK1.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8RQD2;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Van Beilen J.B., Roethlisberger M., Witholt B.;
"Organization of the Pseudomonas putida (oleovorans) GPol and
Pseudomonas putida Pl alkane oxidation genes.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ249793; CAB66148.1; -.
EMBL; P49172; 10TF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8RQD2
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ProDom; PD019232; Tautomerase;
TIGRRAMS; TIGR00013; taut; 1.
SEQUENCE 63 AA; 6996 MW; AJ
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                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                 EMBL; AF134348; AAL83667.1;
                                                                                                                                                                                                                                                                                                           Wessler H.G., Hares D.R., Poulter M.D.,
                                                                                                                                                                                                                                                                                                                                     STRAIN-PAW630;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
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Plasmid pDK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTAX
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Best Local :
                                                               Submitted (JAN-1999) to the EMBL/GenBank/DDBJ EMBL; AF123349; AAD30982.1; -. HSSP; P25685; 1HDJ. InterPro; IPR001623; DnaJ N. InterPro; IPR003095; Hsp_DnaJ. Pfam; PF00226; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                              Mycobacterium xenopi.
Mycobacteria; Actinobacteridae
Bacteria; Firmicutes; Actinobacteridae
Bacteria; Firmicutes; Mycobacteriaceae;
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2002 (TrEMBLrel. 20,
                         PRINTS; PRO0625; DNAJPROTEIN. SMART; SM00271; DnaJ; 1.
                                                                                                                                                                                                                                Brown
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NCBI_TaxID=1789;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. COLUMBIA;
MEDLING=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
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Q9SJH4;
     PROSITE;
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2000) to the EMBL; AC006931; AAD21726.1; SEQUENCE 64 AA; 7401 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=CV. COLUMBIA;
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01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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PS50076; DNAJ_2; 1.
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Pred. No. 7
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7.2e+02;
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Q9TU12;
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Uroplakin 3
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                                                                                                                    STRAIN-NEW ZEALAND WHITE; TISSUE-BLADDER ChO S. K., KWON D.N., Chu H.J., Kim J.H.; Cho S. K. of rabbit uroplakin III cDNA."; Submitted (AUG-1999) to the EMBL/GenBank EMBL; AF178938; AAD55729.1; -.
                                                              SEQUENCE
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Miller S.
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01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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NON_TER 65 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Salmonella typhimurium secreted invasion to Shigella Ipa proteins."; Mol. Microbiol. 18:479-490(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96342378; PubMed=8748032; Hueck C.J., Hantman M.J., Bajaj V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella
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Bacteria; Proteobacteria;
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  7.3e+02;
                  DB 6;
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01-MAR-2002
01-MAR-2002
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01-MAY-2000
01-MAY-2000
01-MAY-2000
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006571;
                                                                        MEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                       SEQUENCE FROM N.A. STRAIN-CDC 1551 / OSHKOSH; Fleischmann R.D., Alland D.,
                                                                 Nature
[2]
                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Last s
01-MAR-2002 (TrEMBLrel. 20, Last a
Hypothetical protein Rv1119c.
RV1119C OR MT1151 OR MTCY22G8.08C.
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KWON D. N., Chu H.J., Cho S.K., Kim J
"Cloning of pig urophakin III cDNA."
Submitted (AUG-1999) to the EMBL/Genl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Cetartioda
NCBI_TaxID=9823;
 Fleischmann R.D., Alland D., Eisen J.A.,
Peterson J., DeBoy R., Dodson R., Gwinn J
Kolonay J.F., Nelson W.C., Umayam L.A.,
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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(TrEMBLrel. 20, Last sequence update)
'TrEMBLrel. 20, Last annotation update)
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7190 MW;
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 Salzberg S.L.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequer
01-MAR-2002 (TrEMBLrel. 20, Last annota
Arylalkylamine N-acetyltransferase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole genome comparison of laboratory strains."; Submitted (APR-2001) to the EMBL; 295585; CAB09051.1; ALEMBL; AE006994; AAK45408.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=21359315; PubMed=11466276;
Mukhopadhyay A.K., Chakraborty S., Takeda Y.,
Mukhopadhyay A
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01-OCT-2000
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                                                                                                                                                                                                      Esox lucius
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al protein;
66 AA; 69;
                                                                                                                                                                                    (Northern pike).
Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Utterback T., Weidman J., Khouri H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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6929 MW; 582B7A7D3C58CF10 CRC64;
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formage (EC 2.3.1.87) (Fragment).
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Last sequence update)
Last annotation updat
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.5e+02;
                                                                                                                                                                                    Vertebrata;
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and CTXphi
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SEQUENCE FROM N.A.

MEDLINE-99185141; PubMed-10085157;
Coon S.L., Begay V., Deurloo D., Falcon
"Two arylalkylamine N-acetyltransferase
synthesis in fish.";
J. Biol. Chem 27.

genes mediate melatonin

Klein

D

Actinopterygii; Esocidae; Esox.

Neopterygii;

Teleostei;

Euteleostei;

Esociformes;

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RESULT
Q95Y38
ID Q9
AC Q9
AC Q9
DT 01
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Best Local :
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007727; OTTEMBLE 04, C:
01-JUL-1997 (TREMBLE 04, L;
01-JUL-1997 (TREMBLE 04, L;
01-MAR-2002 (TREMBLE 20, L;
Hypothetical protein Rv0300.
RV0300 OR MTCY63.05.
                                                   O95Y38, PRELIMINARY; PRT; 74 AA.
Q95Y38; O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 8.3 kDa protein.
Y77E11A.14.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr.
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy.
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                        Hypothetical | SEQUENCE 73
                                                                                                                                                                                                                                                                                                                             Pfam; PF01402; HTH_4;
                                                                                                                                                                                                                                                                                                                                                         EMBL; Z96800; CAB09591.1; -. TubercuList; Rv0300; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF034084; AAD21319.1; -
HSSP; Q29495; ICJW.
ACYLTIANSFERASE; Transferase.
NON_TER 1 1 1
NON_TER 68 68
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Similarity 100.0%;
4; Conservative 0
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3 AA; 8088 MW; 379D16E6EA7D7979 CRC64;
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llarity 100.0%;
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7711 MW;
                       Nematoda; Chromadorea;
            Caenorhabditis
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                      Rhabditida;
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                      Rhabditoidea;
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Q9DHK2
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"Direct Submission.";

Submitted (NOV-2001) to the Elembl; AC024214; AAK67241.1; -

Hypothetical protein.

SEQUENCE 74 AA; 8307 MW;
                                                                                                                                                                                                                                                                    Q9DHK2;
Q9DHK2;
Q1-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                    Thesis (2000), Sir William EMBL; AJ293568; CAC21349.1; SEQUENCE 74 AA; 7905 MW;
                                                                                                                                                                                                                                           111L.
Yaba-like
                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=21176366; PubMed=11277691;
Lee H.J., Essani K., Smith G.L.;
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 Yaba-like disease virus
Viruses; dsDNA viruses,
                                                                                                Lee
                                                                                                                    Lee H.J., Essani K., Smith G.L.;
"The genome sequence of Yaba-like disease virus, a
Virology 281:170-192(2001).
                                                                                                                                                                               Submitted
                                                                                                                                                                                         Lee
                                                                                                                                                                                                                 NCBI_TaxID=132475;
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STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode investigating biology. The C. ele Science 282:2012-2018(1998).
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STRAIN-BRISTOL N2;
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44
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SLDA
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                                  Conservative
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EMBL/GenBank/DDBJ
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                              Score 18; DB 12;
Pred. No. 8.4e+02;
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Pred. No.
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elegans Sequencing
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RESULT

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Q41970;
Q41970;
Q11970;
Q11970
                     Q9LJ84;
Q9LJ84;
Q1-OCT-2000 (
Q1-OCT-2000 (
Q1-DEC-2001 (
Genomic DNA,
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Q53417;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAY-2000
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Desprez T., Amselem J., Chiapello H., Rouze P., Caboche M.,
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; Z18781; CAA79257.1; -.
InterPro; IPR001993; Mitoch_Carrier.
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Mol. Plant Microbe Interact. 7:173-180(1994).
EMBL; S70735; AAB31118.2; -.
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MEDLINE-94281668; PubMed-8012039;
Dockendorff T.C., Sharma A.J., Stacey
"Identification and characterization c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bradyrhizobium japonicum.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
NCBI_TaxID-375;
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Q9AMZ5;
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Q9KAKO;
01-0CT-2000
                                                                                                                                                                      "Complete genome sequence of the alkaliphilic halodurans and genomic sequence comparison wit Nucleic Acids Res. 28:4317-4331(2000).
EMBL; APO01515; BAB06006.1; -.
Complete proteome.
SEQUENCE 76 AA; 8916 MW; 6028CDFC766C6307
                                                                                                                                                                                                                                 STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y.,
Tuji F., Hirama C., Nakamura Y., Og
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                           Bacillus halodurans. Bacteria; Firmicutes;
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01-OCT-2000
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DNA Res. 7:217-221(2000).
EMBL; AP000732; BAB01204.1; -.
SEQUENCE 75 AA; 8777 MW; 5D23536
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                 Saccharum officinarum (Sugarcane).
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Panicoideae; Andropogoneae; Saccharum.
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O81534, O1-NOV-1998 (TIEMBLIEL 08,
O1-NOV-1998 (TIEMBLIEL 08,
O1-JUN-2002 (TIEMBLIEL 21,
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Q47775;
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NCBI_TaxID=4547;
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                                                                                                                                                                                                                                                                                              Submitted (NOV-1995) to the EMBL; D78257; BAA11326.1;
                                                                                                                                                                                                                                                                                                                                                                    Plasmid pYI17.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
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J. Bacteriol. 183:1405-1412(2001).
EMBL; AF322013; AAG60986.1;
SEQUENCE 78 AA; 8994 MW; 8AA5AAF174C86355 CRC64;
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Bacteria; Proteobacteria;
Bradyrhizobium group; Brad
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NCBI_TaxID=1351;
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thes 0;
                              Embryophyta; Tracheophyta;
a; Poales; Poaceae; PACC cl
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                              Poaceae; PACC clade;
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RESULT 36
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Best Local
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Q92KC9;
Q92KC9;
01-DEC-2001 (TremBLrel. 19, La
01-DEC-2001 (TremBLrel. 20, La
01-MAR-2002 (TremBLrel. 20, La
Hypothetical protein R01596,
R01596 OR SMC01197.
                                                          Q42264 PRELIMINARY; PRT; 82 AA. Q42264; Q42264; Q1-NOV-1996 (TrEMBLrel. 01, Created), 01-NOV-1996 (TrEMBLrel. 01, Last sequence up 01-DEC-2001 (TrEMBLrel. 19, Last annotation Carrier protein (Fragment).

Arabidopsis thaliana (Mouse-ear cress).
 NCBI_TaxID=3702; [1]
                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                     Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591787; CAC46175.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 80 AA; 9461 MW; 7C02CD5F7830B99D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            Gapela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Bolstard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont sinorhizobium meliloti strain 1021.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Veronesi C., Thalouarn P.;
"Sugarcane resistance to Striga hermonthica.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF079174; AAC27797.1;
Interpro; IPR001099; N-C_synthase. |
Pfam; PF00195; Chal_stil_synt; 1.
ProDom; PD000453; N-C_synthase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21396507; PubMed=11481430;
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ilarity 100.0%;
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8744 MW;
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Pred. No.
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Pred. | No. 9
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Murphy L., Quail M., Harris U.,
Murphy L., Quail M., Harris U.,
Submitted (JUL-2000) to the EMB
Submitted (JUL-2000) to the EMB
EMBL; Ali6043; CAB97796.1;
InterPro; IPR005141; eRF1_2.
InterPro; IPR005141; eRF1_2.
Pfam; PF03464; eRF1_2; 1.
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Best Local :
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Q9NMB4;
Q1-OCT-2000
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Q1-OCT-2000
Q1-JUN-2002
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Desprez T., Amselem J., Chiapello H., Caboche
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ
EMBL; Z33799; CAA83932.1; -.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mito_carr; 1.
                 Deng C., Davis T.;

Molecular identification of the yellow diploid strawberry: a candidate gene app Theor. Appl. Genet. 0:0-0(2001).

EMBL; AY017485; AAK33142.1; -
                                                                                                                                                                                                                          Chalcone synthase (Fragment).
Fragaria vesca subsp. bracteata.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                                                                                                                                                                                                                                                                           Q94IT9:
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Eukaryota; Eugle
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LM26.178.
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NCBI_TaxID-5664;
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STRAIN=CV. COLUMBIA;
                                                                                                                           STRAIN-CV.
                                                                                                                                            SEQUENCE FROM N.A.
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EMBL/GenBank/DDBJ
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Pred. No. 9.6
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databases.
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STRAIN-950Al; Carroll J.D., Wallace R.C., Keane J., Arbeit R.D.; Carroll J.D., Wallace R.C., Keane J., Arbeit R.D.; "Identification of Mycobacterium avium DNA Sequences the Exported Proteins by Using phoA Gene Fusions."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF143401; AAF74995.1; -.
                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation updat
Exported protein 996A160 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diploid strawberry: a candidate ge Theor. Appl. Genet. 0:0-0(2001). EMBL; AV017477; AAK33134.1; ... InterPro: IPR001099; N-C_synthase. pfam; pF00195; Chal_stil_synt; 1. ProDom; PD000453; N-C_synthase; 1.
                                                                                                                                                                                            Actinomycetales;
NCBI_TaxID=1764;
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Spermatophyta; Magnoliophyta;
eurosids I; Rosales; Rosaceae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00195; Chal_stil_synt; :
ProDom; PD000453; N-C_synthase;
NON_TER 1 1
NON_TER 84 84
                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria;
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Pred. No.
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Pred. No. 9.6e+02;
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eudicots; Rosidae;
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Q93EF2;
01-DEC-2001 (
01-DEC-2001 (
01-DEC-2001 (
                           NON_TER
                                                                              Ge Z., Feng Y., Fox J.G.;
"Helicobacter hepaticus genome: construction of an ordered cosmid
library and sequence analysis of the selected genomic regions.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF358712; AAL16703.1;
                                                                                                                                                                                                        STRAIN=3B1;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
Hypothetical 10.3 kDa protein (Fragment).
Helicobacter hepaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Veronesi C., Labrousse P., Thalouarn P.;
"Histological, physiological and molecular aspects of su
resistance to Orobanche cumana.";
Submitted (JUN 1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF074401; AAC26132.1;
InterPro; IPR001099; N-C_synthase.
Pfam; PPF00195; Chal_stil_synt; 1.
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O81399; O1-NOV-1998 (TREMBLrel. 08, Created)
O1-NOV-1998 (TREMBLrel. 08, Last sequence update)
O1-JUN-2002 (TREMBLrel. 21, Last annotation updat
                                                                  Hypothetical protein.
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               Helicobacter
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NON_TER 1 1
NON_TER 85 85
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SEQUENCE
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les 4; Conservative
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      AA;
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9483 MW;
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406A612F41A3EFD8 CRC64;
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Pred. No. 9.8
); Mismatches
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Pred. No. 9.8e+02;
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A Shukla H.D., Lasky S.P., Mahairas G.G., Berquist B., Pan M., Ranedy S.P., Mahairas G.G., Thorsson V., Sbrogna J., RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S., "Genome sequence of Halobacterium species NRC-1.";
RT "Genome sequence of Halobacterium species NRC-1.";
RT "Genome sequence of Halobacterium species NRC-1.";
RT Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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Matches 4
[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE=21608550; PubMed=11743193; ,
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P.,
Gord
Raymond C., Tao Y., Biddle P., Jung M., Krespan W., Perry
The Company R., Kim S., Hendrick C., Zhao Z.-Y., Dolan
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Best Local (
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence of the control of the co
                                                                                                                                                                                                                                                                                                                                   Agrobacterium tumefaciens
Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
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VNG0025H.
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Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Halobacterium.
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01-MAR-2001
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4; Conservative
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Pred. No. 1e+
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rision; Rhizobiaceae
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Q9NMI
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Job time : 23.3333 secs
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Best Local Similarity
Matches 4; Conserve
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Q9NMI7;
01-OCT-2000
01-OCT-2000
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 9.8 kDa protein (Fragment).
LM26.105.
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EMBL; AE008986; AAL41144.1; -.
EMBL; AE007953; AAK85939.1; -.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
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"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
Science 294.2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-FRIEDLIN;
MUTPHY L., Quail M., Harris
Submitted (JUL-2000) to the
EMBL; AL160493; CAB97723.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
NCBI_TaxID=5664;
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"The genome of the natural genetic engineer Agrobacterium tumu C58.";
Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
NON_TER 89 89
SEQUENCE 89 AA; 9751 MW;
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13 SLDA 16
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Pred. No. 1e+03;
Mismatches
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                           Score
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     PAT943-5
23
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Match
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1: /SIDS2/gcgdata/c
2: /SIDS2/gcgdata/c
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19.150 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compuç
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AAW38119
AAE01065
AAY49212
ABB39349
AAM60026
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ABG42450
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                                                    Peptide #6855 enco
                                                                                                                                                                                                       Description
                   Human brain expres
Human peptide enco
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AAW62372	AAB90483	AAB90383	AAB90304	AAB90303	AAB90302	AAB90301	ABP09824	AAB90300	AAB90299	AAB90298	AAG78507	AAB90297	AAB90296	AAB90295	AAB90294	AAB90293	AAB90292	AAB90291	AAB90290	AAB90289	AAB90288	AAB90287	AAB90286	AAB90285	AAY12228	ABG37890	AAM03882	64	AAM16152	AAM68335	AAM55966	205	3513	ABB29961
hromb	SAA	SAA			Human SAA carboxy	Human SAA carboxy	Human ORFX protein	Human SAA carboxy	Human SAA carboxy		Mouse serum amyloi	SAA	Human SAA carboxy	Human SAA carboxy		Human SAA carboxy	SAA	Human SAA carboxy		Human SAA carboxy	Human SAA carboxy	Human SAA carboxy		Human SAA carboxy	Human 5' EST secre	eptide	Peptide #2564 enco	#2682	de #25		rain ex	#256	#2645	Peptide #2612 enco

ALIGNMENTS

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RESULT 1
AAB35994
WPI; 2000-687351/67.
                                       Choi E,
                                                                                                                       02-NOV-2000.
                                                                                                                                       WO200065066-A1
                                                                                                                                                      Gluconobacter oxydans.
                                                                                                                                                                     Sorbitol dehydrogenase; SDH; Gluconobacter oxydans; D-sorbitol; L-sorbose production; 2-keto-L-gulonic acid.
                                                                                                                                                                                               Sorbitol dehydrogenase subunit 2 internal peptide.
                                                                                                                                                                                                                01-MAR-2001
                                                                                                                                                                                                                                ААВЗ5994;
                                                                                                                                                                                                                                              AAB35994 standard; Protein; 7 AA
                                                       (LEEE/)
                                                             (CHOI/) CHOI E.
(RHEE/) RHEE S.
                                                                                      23-APR-1999;
                                                                                                       23-APR-1999;
                                                      LEE E.
                                      Rhee S,
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Novel membrane-bound sorbitol dehydrogenase nucleic acid molecule isolated from Gluconobacter suboxydans useful for the fermentative

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Best Local Similarity
                                                                                                          An antibody capable of recognising Amyloid A and this peptide but which does not react with other specified peptides (see AAP82046-9) is useful for detection of secondary amyloidosis
                                                                                          Sequence
                                                                                                                                                                                     Anti-amyloid-A protein monoclonal antibody used esp for detection of sec amyloidosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dehydrogenase (SDH) from Gluconobacter oxydans. The invention includes polynucleotides (AAC83153 - AAC83154) encoding the 3 subunits of SDH (AAB35987 - AAB35989). Also included in the invention are two polynucleotide sequences AAC83156 and AAC83157 which contain the subunit coding regions. The sorbitol dehydrogenase polynucleotide sequences are useful for producing L-sorbose from D-sorbitol and for increasing the production of 2-keto-1-gulonic acid by transforming a host cell, especially Gluconobacter with the DNA and selecting the transformed host cell. The present sequence represents the SDH subunit 2 internal
                                                                                                                                                               Claim 2; Page 649;
                                                                                                                                                                                                                         WPI; 1988-094820/14.
                                                                                                                                                                                                                                                                                                                                                                    synthetic
                                                                                                                                                                                                                                               (KYOW ) KYOWA HAKKO
                                                                                                                                                                                                                                                                       13-AUG-1986;
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                                                                                                                                                                                                                                                                                                                                             JP63044895-A.
                                                                                                                                                                                                                                                                                                                                                                                    Amyloid A protein; secondary amyloidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                        19-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP82045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP82045 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to an isolated membrane-bound sorbitol dehydrogenase (SDH) from Gluconobacter oxydans. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                 "Peptide 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 2-keto-L-gulonic acid and L-sorbose from D-sorbitol
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            consisting of residues 37-47 of amyloid A protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Pred. No.
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Pred. No. 7.8e+05;
); Mismatches 0;
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RESULT 3
ANY32231
ID ANY3
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AAW38119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
Peptide recognition unit; WW domain; cell signalling; growth r cytoskeleton organisation; targeted drug screening; modulator; WW domain interaction; YAP protein; dystrophin; epithelial sodium channel protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents complementarity determining region 3 (CDR3) of the heavy chain variable region of murine monoclonal antibody mAb174-74-11. This antibody is an example of an agonist molecule that specifically binds to or interacts with human granulocyte colony stimulating factor (G-CSF) receptor to stimulate cell proliferation and differentiation, especially by dimerising the receptor or activating phosphorylation of kinases associated with the receptor. Agonist antibodies can be used to stimulate proliferation of G-CSF-dependent cells, e.g. to differentiate leading to a repopulation of neutrophilic granulocyte lineage cells, especially to treat neutropenia (claimed). They can also be used to detect human G-CSF receptor immunologically.
                                                                                                                                           PPPPY motif containing peptide ENaC-beta.
                                                                                                                                                                                                                                                                AAW38119;
                                                                                                                                                                                                                                                                                                              AAW38119 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment of neutropenia by stimulating proliferation of neutrophilic cell lineage progenitors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; Page 30; 64pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Granulocyte colony stimulating factor receptor; G-CSF;
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Pred. No.
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                                                                                    cell signalling; growth regulation;
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37;
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                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptides AAW38115-28 are derived from epithelial sodium channel alpha (ENaC-alpha), beta (ENaC-beta) and gamma (ENaC-gamma) proteins. The peptides contain ppppy-like motifs, which are found in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides containing this residue bind to the YAP WW domain, but not the WW domain from dystrophin or to a panel of SH3 domains. Peptides AW388115-28 were biotinylated and complexed with alkaline streptavidin, and used in a cross affinity mapping experiment. They were tested for their ability to bind to the 3 individual novel WW domains of WWP4 (AAW36797), which were expressed as glutathione-S-transferase expression proteins. The present peptide binds to some of the WW domains of the WW4 protein. The WW domain is a small functional domain. Its name is derived from the observation that two tryptophan residues, one in the amino terminal portion of the WW
                                                                                                                                                                                                                                                                                                                                                                    and growth regulation or the organisation of the cytoskeleton.

Polypeptides containing a WW domain are identified by treating a multivalent recognition unit complex that has selective binding affinity for a WW domain, with many polypeptides and identifying those with selective affinity for the complex. Proteins containing WW domains are used for targeted drug screening, i.e. to identify potential modulators of specific WW domain interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying cell signalling and growth regulatory polypeptides by reaction with multivalent recognition complex - polypeptides are useful in targetted drug selection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain and one in the carboxyl terminal portion, are conserved. Most proteins containing WW domains have a function involving cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CYTO-) CYTOGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09737223-A1
Horse; colostrum; serum amyloid A; SAA; antibacterial; antidiarrhoeic;
                               Horse colostrum-associated serum amyloid A (SAA) peptide #3
                                                                  17-JUL-2001
                                                                                                AAE01065
                                                                                                                            AAE01065 standard;
                                                                                                                                                                                                             7
                                                                                                                                                                                                                                           1 NYDA 4
                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                           NYDA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.3;
                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                         13 AA;
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 24B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kay BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NORTH CAROLINA
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0630916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US05547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "PPPPY motif"
                                                                                                                            peptide;
                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pirozzi
                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                         Score 23; DB
Pred. No. 45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ن</u>
                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                       Length 13;
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                          0;
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RESULT 6 AAY49212

H

AAY49212 standard;

peptide;

19

07-FEB-2000

(first entry)

Seq ID No:

6 of US5977316

Monoclonal antibody; MAb; 1A7; GD2; immune response; melanoma; neuroblastoma; glioma; soft tissue carcinoma; small cell carcitumor-associated antigen.

small cell carcinoma;

US5977316-A Unidentified 밁 Qy

N NYDA 5

0;

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Matches
                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                              The patent discloses novel colostrum-associated Serum Amyloid A (SAA) from mammals. SAAs are small apolipoproteins that accumulate and associate rapidly with high-density lipoprotein 3 (HDL3) during the acute phase of inflammatory response. They are characterised by the TFLK motif in the N-terminal region which has the ability to stimulate mucin 3 (MUC3) production. Colostrum associated SAAs are used to prevent or treat infectious diseases associated with enteric pathogens (particularly Escherichia coli) such as traveller's diarrhoea, infant diarrhoea, necrotising enterocolitis (NEC), urinary tract infections, and infectious diarrhoea in herd animals. They are used to prevent dysentery and other infectious diseases particularly for the military.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    apolipoprotein; inflammatory response; mucin 3; MUC3; therapy; Escherichia coli infection; traveller's diarrhoea; infant diarrhoea; necrotising enterocolitis; NEC; urinary tract infection; dysentery; infectious diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 20; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New colostrum-associated serum amyloid A protein induces mucin production in epithelial cells and is useful to prevent and treat enteric pathogen infection \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-308640/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McDonald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-1999; 99US-0425679
14-JUL-2000; 2000US-0218482
17-JUL-2000; 2000US-0218611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200131006-A2
                                                                                                                                                               Sequence
                                                                                                                                                                                                                 The present sequence peptide from horse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYNE-) UNIV NEBRASKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-OCT-2000; 2000WO-US29065
                                                                              Local
1 NYDA 4
                                                  Similarity 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TL,
                                                                                                                                                               13 AA;
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weber A,
                                                                           100.0%;
                                                                                                                                                                                                                                             is colostrum-associated serum amyloid A (SAA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mack DR,
                                                     0,
                                                                              Pred. No.
                                                                                                          Score 23;
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Larson MA;
                                                                              45;
                                                                                                          DB 22;
                                                     0
                                                                                                    Length 13;
                                                       Indels
                                                     0;
                                                     Gaps
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RESULT 7
ABB39349
ID ABB3
XX ABB3
AC ABB3
XX ABB3
AC ABB3
XX Home
XX H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                    04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides a monoclonal antibody (MAb) designated 1A7, which elicits an anti-GD2 (tumor-associated antigen) immunological response in humans. MAb 1A7 has defined light and heavy chain variable region sequences. The MAb 1A7 and polypeptides can be used for eliciting an anti-GD2 immune response. The polypeptides can also be used for detecting or purifying anti-GD2 antibody. The products can be used for treating GD2 -associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue carcinoma, and small cell carcinoma. They can be used for palliating the disease or for reducing the risk of recurrence. Sequences MAX49212-216 represent fragments used for comparison with the light chain variable region of MAb 1A7.
                        Penn SG
                                                                                                                                        21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                            30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                      WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB39349 standard; Peptide; 28 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody 1A7 which elicits an anti-GD2 immunological response, useful for the development of products for the detect treatment of cancers - \,
                                                                    (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; foetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB39349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-619711/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KENT ) UNIV KENTUCKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NYDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΚA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #6855
                                                                 MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chatterjee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19
                                                                                                             2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0234263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 3B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                       2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0372676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0591196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bу
                     Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human foetal liver single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chatterjee
                     Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23;
Pred. No.
                     Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
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RESULT 8
AAM60026
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Matches
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                                                                                                                                                          04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exo nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                 WPI; 2001-483446/52
                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                                              WO200157275-A2
                                                                                                                                                                                                                                                                                                                              microarray; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                         Human brain expressed single exon probe encoded
                                                                                                                                                                                                                                                                                                                                                                               05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                   AAM60026;
                                                                                                                                        (MOLE-)
                                                                                                                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                     epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                        Human;
                                                                                                                                                                                                                                                                                                                                                                                                                    AAM60026 standard; Protein; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human [fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         measuring human gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity es 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NYDA 4
                                                                                                                     SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NYDA 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                                                                                                                                       brain expressed
                                                                                                                                       MOLECULAR DYNAMICS INC.
                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
                                                                                                                                                                   2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                            2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO 31984; 639pp + sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                   Chen W,
                                                                                                                                                                                                                                                                                                                             exon; gen
s disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                            gene expression analysis;
se; multiple sclerosis; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                    Rank | DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from human foetal
                                                                                                                                                                                                                                                                                                                            s; probe;
schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                          SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                           NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
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0;

probes which are derived from genor brain. They can be used to measure which may enable the diagnosis and

Example

4;

SEQ ID NO:

exon nucleic acid

probes

for analyzing gene expression

in

human

The present invention provides a number of single exon nucleic acid

from genomic sequences expressed in the

gene expression improved

in

brain cell

samples human 32131; 650pp + Sequence Listing; English

diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of

probes

of the

invention.

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RESULT 9
AAM72626
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                                         Query Match
Best Local S
Matches 4
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Best Local Similarity
                                                                                                                                                                                                                                                                                                 04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0632366.
21-SEP-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                    probes which are derived from genomic sequences expressed in the bone marrow. They can be used to measure gene expression in bon samples, which may enable the improved diagnosis and treatment such as lymphoma, leukaemia and myeloma. The present sequence i protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                     WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM72626 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                  Sequence
                                                                                                                                                          The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM72626;
                                                                                                                                                                                                                                                                              (MOLE-)
                                                   Local Similarity
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                    1 NYDA 4
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|NYDA 10
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                                                                                                                                                                                                    genome-derived single exon nucleic acid probes useful
zing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bone marrow expressed probe encoded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.
                                                                                                                                                                                                                                                                              MOLECULAR DYNAMICS INC
                                                                                                                                                                                SEQ
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                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leukaemia; lymphoma; myeloma.
                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                          Chen
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                                                                                                                                                                              658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 22
Pred. No. 1e+02;
                                                   Score 23; DB 22
Pred. No. 1e+02;
                                                                                                                                                                                                                                                          Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                          Mismatches
                                                                                                       The present sequence is the invention.
                                                                                                                          quences expressed in the human
gene expression in bone marrow
lagnosis and treatment of cancers
                                                             22;
                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                            Length 28
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CC probes: Also included are a microarray comprising the novel set of converse the novel set of probes which hybridise at high stringency to a concleic acid expressed in the human lung; measuring gene expression in a cC sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung (mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the exons from genomic sequence by the method constraints and the exons in the exons in several ctissues and/or cell types using hybridisation to a single exon for expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the method are probes/open reading frames (ORF). The probes are used for gene

for

particularly

The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614

of.

Claim 27;

SEQ ID No 32115; 634pp; English.

Spatially-addressable set of single exon nucleic acid probes, used

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expression

in

human

lung samples

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RESULT 10
ABG42450
AC ABG42
XX Human
XX Human
XX Human
XX Human
XX Human
XX Homo
XX Pullac
XX Pullac
XX Pullac
XX Pullac
XX ABG42
XX WO200
XX WO1;
XX O4-FP
PR 26-M
PR 27-S:
PR 21-S:
P
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Nlemann-Pick disease; tuberous sclerosis; Gaucher's disease; Nlemann-Pick disease; pulmonary hadnosiderosis; pulmonary hadnosiderosis; pulmonary hadnosiderosis; pulmonary histicocytosis; lymphangiolelomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-180312P.
2000US-207456P.
2000US-0608408.
2000US-0632366.
2000US-234687P.
2000US-236359P.
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RESULT 11
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part
                     The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label
                                                                                                                                                                    Claim
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26-MAY-2000; 2000US-0207456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmon fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonare disease, pulmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 using human lung such as asthma,
                                                                                                                                                                                                                                                                                                                                                            Penn
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                                                                                                                                                                                                                comprises number of
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC
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2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                  12929;
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                                                                                                                                                                                                                                                                                                                                                         Chen
                                                                                                                                                                                                             e set of single exon nucleic acid probes,
e expression in sample derived from human
of single exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                                                         Σ,
  breast, and microarray.
                                                                                                                                                             327pp
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Pred.
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probes
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Best Local
                                                                                                                                                                                                                                                                                                             30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                             measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in sample derived from human fetal liver. The present sequence is a peptide encoded by a single exonucleic acid probe of the invention.
Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical
                                                                                                                                                              analyzing
                                                                                                                                                                                                                                 Penn
                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide #2645 encoded by human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000;
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                                                                                                                                                                                                                                 SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form ped specification, but was obtained in electronic wife at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                     27;
                                                                                                                                                                            genome-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toetal
                                                                                                                                                                                                                                                           MOLECULAR DYNAMICS INC.
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                                                                                                                                     SEQ
                                                                                                                                                              gene
                                                                                                                                                                                                                                Hanzel DK,
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; 2000US-0207456.
; 2000US-0608408.
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2000US-0234687.
2000US-0236359.
2000US-0024263.
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                                                                                                                                     ID NO 27774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     liver; gene expression; single exon nucleic acid probe-
                                                                                                                                                              expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                           single exon
                                                                                                                                                                                                                                Chen W,
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                                                                                                                                   639pp + sequence listing; English
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                                                                                                                                                               human
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                                                                                                                                                                                                                                 Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              foetal liver single exon probe.
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                                                                                                                                                                           nucleic
                                                                                                                                                               fetal
                                                                                                                                                              acid probes useful for liver -
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                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234589.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire value in the proposition of the printed specification, but was obtained in electronic format directly from WIPO at fire value in the proposition of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           congenital heart disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
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                                                                                                                                                                   36 AA;
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                                                       Conservative
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                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes for analyzing gene expression
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Pred. No. 1.4e+02;
                                                                           Score 23; DB 22;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank
                                                       Mismatches
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                                                                                                      Length 36;
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                                                    Indels
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RESULT 15
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                             The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, enilensy and cancers. The present sequence is a protein encoded by one of
                     06-NOV-2001
                                                             AAM68335 standard;
                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                    epilepsy and cancers. The present sequence is a protein encoded the probes of the invention.
                                                                                                                                                                                                                                                                                                                                       Single exon
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04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epilepsy;
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epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human brain
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2000US-0207456.
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2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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                   (first entry)
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                                                                                                                                                                    Score 23;
Pred. No.
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                                                                                                                                                           Mismatches
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                                                                                                                                                                     1.4e+02;
                                                                                                                                                                                DB 22;
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Human bone marrow expressed probe encoded protein SEQ ID

NO:

28641.

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RESULT 16
AAM16.152
ID AAM16
XX AAM16
AC AAM16
AC AAM16
AC Pepti
XX Probe
KW Probe
KW Cerv
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PN WO20
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PD 09-A
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Best Local S
Matches 4
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26-MAY-2000;
30-JUN-2000;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                  09-AUG-2001.
                                                                                      WO200157278-A2
                                                                                                                                      Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                            30-JAN-2001;
                                                                                                                                 cervical
                                                                                                                                                               Peptide #2586 encoded by
                                                                                                                                                                                        12-OCT-2001
                                                                                                                                                                                                                                 AAM16152 standard; Protein;
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04-OCT-2000;
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microarray; cancer;
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zing gene expression in human bone marrow -
                                                                                                                                 cancer.
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2000US-0180312.
2000US-0207456.
2000US-0608408.
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                           2001WO-US00670.
                                                                                                                                                                                       (first
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2000US-0207456.
                                                                                                                                                                                                                                                                                                                                                                            AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO:
                                                                                                                                                                                      entry)
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; leukaemia;
                                                                                                                                                                                                                                                                                                                                100.0%; S
100.0%; F
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28641; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen
                                                                                                                                                                probe
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                                                                                                                                                                                                                                  36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                          Score 23; DB 22;
Pred. No. 1.4e+02;
                                                                                                                                                           for measuring cervical gene expression
                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphoma; myeloma
                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                    Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
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RESULT 17
AAM28645
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Best Local
                                                                                                                                     04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0632366.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
WPI; 2001-488897/53.
                                              Penn
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; microarray; human; placenta; lantenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microraarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                        (MOLE-)
                                                                                                                                                                                                                                                                                                                                30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #2682 encoded by probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM28645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM28645 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly from the specification of the sequence of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human cervical epithelial cell:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn
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                                            SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-488901/53.
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                                                                                           MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
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                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ယ
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ilarity 100.0%;
Conservative C
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; 2000US-0234687.
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; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No 20978; 487pp; English.
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                                            Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23; DB 22;
Pred. No. 1.4e+02;
Mismatches 0;
                                            Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 18
AAM03882
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
The present invention relates to novel single exon nucleic acid probes (see Aa10010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                    Novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing
                                                                                                                                                                                                                                                                                                                               Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                  (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-2000
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                                                                                                                                                                                                                                                                                            2001-476286/51
                                                                                                                                                                                               27;
                                                                                                                                                                                                                                   single exon nucleic acid probe used human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome-derived single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS
                                                                                                                                                                                            SEQ ID No 12622; 322pp; English
                                                                                                                                                                                                                                                                                                                               Hanzel
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                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0180312.
2000US-0207456.
2000US-060840B.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease; proliferative breast disease; non-carcinoma tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast
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                                                                                                                                                                                                                                                                                                                             DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease; breast cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe
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Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                               Rank DR;
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                                                                                                                                                                                                                                                    measuring
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probes (SENP: encoded by one
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                                                                                                                                                                                                                                                    expression
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung

Claim

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No

634pp; English.

measure gene expression in human lung

2002-114183/15.

Spatially-addressable set of single exon nucleic acid probes,

samples

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RESULT 19
ABG37890
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                                                                                                                                                                       Penn
                                                                                                                                                                                                                                      30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                         04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                         15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                    chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Nlemann-tick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; pulmonary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; single exon probe; asthma; lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human peptide encoded by genome-derived single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              breast disease and non-carcinoma tumours.
Note: The sequence data for this patent did no specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                        (MOLE-)
                                                                                                                                                                                                                   21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00665
                                                                                                                                                                                                                                                                                                                           WO200186003-A2
                                                                                                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                               hyaline membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG37890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG37890 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                              sapiens
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                                                                                                                                                                                        MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                       Hanzel
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2000US-0632366.
2000US-234687P.
2000US-236359P.
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                                                                                                                                                                                                                                                                 2000US-180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                         2000US-207456P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                      DK,
                                                                                                                                                                                                                                                                                                                                                                disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide;
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                                                                                                                                                                      Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred.
                                                                                                                                                                       Rank
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                                                                                                                                                                       DR
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                                                                                                                                                                                                                                                                                                                                                                                                                                         COPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID 27555
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RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal paptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostat
       Duclert
                                                                         (GEST ) GENSET
                                                                                                                                           01-AUG-1997;
                                                                                                                                                                                                             31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiccytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reproductive hormone regulation; thrombolytic; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human 5' EST secreted protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY12228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY12228 standard; Protein; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NYDA 4
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       A,
Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                             98WO-IB01238
                                                                                                                                           97us-0905134
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100.0%; P
ative 0;
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Pred. No. 1.4e+02;
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'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour
Lacroix
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the probe is included
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  haemostatic;
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RESULT 21
AAB90285
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                      Human;
FPRL1;
                                  WPI; 2001-211457/21
                                                                                                                                                                                                                                                                                      antiatherosclerotic; immunosuppressive;
immune system disorder; amyloidosis; inf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating activity tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into
New serum amyloid A and formyl peptide receptor variant complex and its
                                                             Wang J,
                                                                                                                                                      22-SEP-1999;
                                                                                                                                                                                                               W0200121188-A1
                                                                                                                                                                                                                                                                                                                                                                Human SAA carboxy truncation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX40826 to AAX41093 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAY01602 and AAX11994 to AAX12260, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene
                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB90285 standard; Protein; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acids encoding human secreted proteins - obtained cDNA libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle and heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX41061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 NYDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NYDA 4
                                                                                                                                                                                                                                                                         rejection;
                                                                                                                                                                                                                                                                                                                   immunomodulatory; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                    serum amyloid A; SAA; human
                                                                                             SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                             Oppenheim JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42
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                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                         99WO-US21770
                                                                                                                                                    99WO-US21770.
                                                                                           HEALTH & HUMAN
                                                                                                                                                                                                                                                                         arthritis; atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO: 43.
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Pred. No.
                                                                                        SERVICES
                                                            Gong W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                              formyl peptide receptor variant;
mmatory; antimicrobial; antiarthritic;
sive; SAA/FPRL1 complex; cancer;
                                                                                                                                                                                                                                                                                    inflammation; infection;
                                                            Gao J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                            Murphy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 42;
                                                             PM
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RESULT 22
AAB90286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprises a peptide agent with a sequence corresponding to SAA, or its conservative variant or functional fragment, bound to FPRL1. Modulators of the SAA/FPRL1 complex are useful for treating immune system
            The present sequence is a fragment of human serum amyloid A (SAA). Invention relates to the discovery that SAA is a ligand for FPRL1 (formyl peptide receptor variant). A complex has been isolated that comprises a peptide agent with a sequence corresponding to SAA, or conservative variant or functional fragment, bound to FPRL1. Modula of the SAA/FPRL1 complex are useful for treating immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                        New serum amyloid A and formyl peptide receptor variant complex and its modulators, useful for treating immune system disorders, amyloidosis, inflammation, infection, organ rejection, arthritis, atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
immune system disorder; amyloidosis; inflammation; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders, amyloidosis, inflammation, infection, organ rejection, arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a fragment of human serum amyloid A (SAA). invention relates to the discovery that SAA is a ligand for FPRL1 (formyl peptide receptor variant). A complex has been isolated that
                                                                                                                 Disclosure; Page 15; 141pp; English
                                                                                                                                                                                                                                                                                                          22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                       22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human SAA carboxy truncation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB90286 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modulators, useful for treating immune system disorders, amyloidosis, inflammation, infection, organ rejection, arthritis, atherosclerosis
                                                                                                                                                                                                                                                                            (USSH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; serum amyloid A; SAA; human formyl peptide receptor variant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42
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                                                                                                                                                                                                                       2001-211457/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                      rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                 Oppenheim JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ability
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                         99WO-US21770
                                                                                                                                                                                                                                                                                                                                     99WO-US21770
                                                                                                                                                                                                                                                                            HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        arthritis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modulate assembly of the SAA/FPRL1 complex.
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                                                                                                                                                                                                                                                 SuS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .08;
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Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:
                                                                                                                                                                                                                                                 Gong W,
                                                                                                                                                                                                                                                                             SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                               Gao J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
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organ
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                                                                      for FPRL1 (hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                            Modulators
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                                                                     (human
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42

NYDA 45

1 NYDA 4

Matches

4;

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Gaps

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RESULT 23
AAB90287
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Best Local
             Query Match
Best Local
                                                                     The present sequence is a fragment of human serum amyloid A (SAA). The invention relates to the discovery that SAA is a ligand for FPRLI (human formyl peptide receptor variant). A complex has been isolated that comprises a peptide agent with a sequence corresponding to SAA, or its conservative variant or functional fragment, bound to FPRLI. Modulators of the SAA/FPRLI complex are useful for treating immune system disorders, amyloidosis, inflammation, infection, organ rejection, arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested for their ability to modulate assembly of the SAA/FPRLI complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic; antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer; immune system disorder; amyloidosis; inflammation; infection;
                                                 Sequence
                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                         modulators, useful inflammation, infec
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                                                                                                                                                                                                                             and neoplasia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rejection; arthritis;
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              Similarity
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                                                   47 AA;
                                                                                                                                                                                                                                                                                                                                             DEPT HEALTH & HUMAN SERVICES.
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100.0%; ilarity 100.0%; Conservative
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             Score 23;
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No.
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              1.8e+02;
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AAB90288
ID AAB90
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KW FPRL1
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YX WO200
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PD 29-MA
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Best Local
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                                                                                        Human SAA carboxy truncation, SEQ ID NO: 47.
                                                                                                                                                         01-JUN-2001
                                                                                                                                                                                                               AAB90289;
                                                                                                                                                                                                                                                          AAB90289 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New serum amyloid A and formyl peptide receptor variant complex and its modulators, useful for treating immune system disorders, amyloidosis, inflammation, infection, organ rejection, arthritis, atherosclerosis and neoplasia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-SEP-1999;
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ues 4; Conserv
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serum amyloid A; SAA; human formyl peptide receptor variant; immunomodulatory; antiinflammatory; antimicrobial; antiarthr
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100.0%; F
|tive 0;
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                                                                                                                                                                                                                                                             49
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Pred. No. 1.9
); Mismatches
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. 1.9e+02;
ches 0;
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  antiarthritic;
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RESULT 26
AAB90290
ID AAB90
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                                                                                                                                                                                                                               Human; serum amyloid A; SAA; human formyl peptide receptor variant; FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic; antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer; immune system disorder; amyloidosis; inflammation; infection;
22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a fragment of human serum amyloid A (SAA). The invention relates to the discovery that SAA is a ligand for FPRL1 (huma formyl peptide receptor variant). A complex has been isolated that comprises a peptide agent with a sequence corresponding to SAA, or its conservative variant or functional fragment, bound to FPRL1. Modulators of the SAA/FPRL1 complex are useful, for treating immune system disorders, amyloidosis, inflammation, infection, organ rejection, arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested for their ability to modulate assembly of the SAA/FPRL1 complex.
                                         22-SEP-1999;
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                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                               Human SAA carboxy truncation,
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immune system disorder; amyloidosis; inflamm
organ rejection; arthritis; atherosclerosis.
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Pred. No. 1.9e+02;
Mismatches 0;
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a fragment of human serum amyloid A (SAA). The invention relates to the discovery that SAA is a ligand for FPRLI (huma formyl peptide receptor variant). A complex has been isolated that comprises a peptide agent with a sequence corresponding to SAA, or its conservative variant or functional fragment, bound to FPRLI. Modulators of the SAA/FPRLI complex are useful for treating immune system
                                                                                                                                                                                                                                                                                                  Human; serum amyloid A; SAA; human formyl peptide receptor variant; FPRLI; immunomodulatory; anttinflammatory; antimicrobial; antiarthritic; antiatherosclerotic; immunosuppressive; SAA/FPRLI complex; cancer; immune system disorder; amyloidosis; inflammation; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders, amyloidosis, inflammation, infection, organ rejection, arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested for their ability to modulate assembly of the SAA/FPRL1 complex.
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                                                                                                                                                                                     22-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                 Human SAA carboxy truncation,
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                                                                                                                                                                                                                                                                                                                                                                                                                     AAB90291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modulators, useful
                                inflammation,
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                                                                                                          Wang J,
                                                                                                                                                                                                                                                               Homo sapiens.
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                              serum amyloid A and formyl peptide receptor variant complex and its ulators, useful for treating immune system disorders, amyloidosis, lammation, infection, organ rejection, arthritis, atherosclerosis
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                                                                                                                                                                                                                                                                                        rejection;
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                                                                                                          Oppenheim JJ,
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                                                                                                                                                                                                                                                                                        arthritis;
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ative 0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO: 49.
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thes 0;
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Disclosure; Page 15; 141pp; English

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AAB90292
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                                                            The present sequence is a fragment of human serum amyloid A (SAA). The invention relates to the discovery that SAA is a ligand for FPRLI (human formyl peptide receptor variant). A complex has been isolated that comprises a peptide agent with a sequence corresponding to SAA, or its conservative variant or functional fragment, bound to FPRLI. Modulators of the SAA/FPRLI complex are useful for treating immune system
                          disorders, amyloidosis, inflammation, infection, organ rejection, arthritis, atherosclerosis and neoplasia. Fragments of SAA were t for their ability to modulate assembly of the SAA/FPRL1 complex.
                                                                                                                                                              Disclosure; Page 15; 141pp; English.
                                                                                                                                                                                                                   New serum amyloid A and formyl peptide receptor variant complex and its modulators, useful for treating immune system disorders, amyloidosis,
                                                                                                                                                                                                                                                                                         Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiatherosclerotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens.
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                                                                                                                                                                                              infection,
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Pred. No.
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the SAA/FPRL1
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AAB90293
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Best Local
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AAB90294 standard; Protein;
                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; ca
immune system disorder; amyloidosis; inflammation; infection;
organ rejection; arthritis; atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                 and neoplasia
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                                                                                                                                                                                                                                                                                                                                                                                                                   Wang J,
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100.0%; P
Live 0;
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antiinflammatory;
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54 AA
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Pred. No. 2.1e+02;
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Pred. No.
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RESULT 31
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                  antiatherosclerotic; immunosuppressive;
immune system disorder; amyloidosis; inf
                                                                                                                         Human
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                                                                                                                                                                                                      AAB90295;
                                                                                                                                                                                                                                         AAB90295 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                            NYDA 45
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    rejection; arthritis;
                                                                                                                    SAA carboxy truncation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rejection;
                                                             immunomodulatory; antiinflammatory;
                                                                           serum amyloid A; SAA; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                serum amyloid A; SAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oppenheim JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 16; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erotic; immunosuppressive; SAA/FPRL1 complex; cancer; disorder; amyloidosis; inflammation; infection; on; arthritis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US21770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US21770.
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory;
atherosclerosis
                                                                                                                                                                                                                                           55
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human
                                                                                                                    SEQ ID NO: 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 22;
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gongl W,
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                              formyl peptide receptor variant;
mmatory; antimicrobial; antiarthritic;
sive; SAA/FPRL1 complex; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |formyl peptide receptor variant;
mmatory; antimicrobial; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID NO:
                    inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murphy PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           54;
                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulators
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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